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OM protein - protein search, using sw model

Run on: June 12, 2003, 08:45:11 ; Search time 38 Seconds

(without alignments)  
1413.158 Million cell updates/sec

Title: US-09-412-100-23

Perfect score: 2079

Sequence: 1 MSMTSGICASTMQISIGCA.....DAMAGDAINNALGKLGAA 403

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	100.0	403	19	AAW5863
2	2079	100.0	403	19	AAW62455
3	2079	100.0	403	19	AAW61114
4	2079	100.0	403	20	AAW87639
5	2079	100.0	403	21	AAW71093
6	2079	100.0	403	21	AAW84854
7	2079	100.0	403	22	AAW6710
8	2079	100.0	403	23	ABW09225
9	2079	100.0	403	23	AAE18295
10	2079	100.0	403	23	AAE16447

11	1928	92.7	385	18	AAW06598
12	1913	92.0	385	15	AAW45751
13	718.5	34.6	338	18	AAW06597
14	718.5	34.6	338	20	AAW87638
15	718.5	34.6	338	20	AAW82407
16	718.5	34.6	338	21	AAW71092
17	718.5	34.6	338	21	AAW84853
18	718.5	34.6	338	21	AAW5801
19	718.5	34.6	338	22	AAW06709
20	718.5	34.6	338	23	AAW09224
21	718.5	34.6	338	23	AAE18294
22	718.5	34.6	338	23	AAW5862
23	718.5	34.6	340	19	AAW5862
24	718.5	34.6	340	19	AAW61113
25	713.5	34.3	340	19	AAW62454
26	226.5	10.9	898	18	AAW31853
27	222	10.7	272	22	ABW70198
28	215.5	10.4	718	12	AAW14308
29	211.5	10.2	651	20	AAW40097
30	211.5	10.2	651	23	AAW11781
31	211.5	10.2	718	19	AAW53346
32	211.5	10.2	718	21	AAW59070
33	206	9.9	604	16	AAW9057
34	204	9.8	528	22	AAW82611
35	203.5	9.8	318	21	AAW81229
36	202	9.7	630	23	AAW50042
37	202	9.7	676	23	AAW50047
38	202	9.7	989	23	AAW50038
39	202	9.7	1255	23	AAW50037
40	202	9.7	1880	23	AAW50039
41	200	9.6	388	20	AAW04999
42	199.5	9.6	201	21	AAW31750
43	198.5	9.5	738	19	AAW56163
44	198.5	9.5	3190	22	AAW84634
45	198.5	9.5	3275	22	ABW70437

#### ALIGNMENTS

RESULT 1  
AAW5863  
ID AAW5863 standard; Protein; 403 AA.  
XX  
AC AAW5863;  
XX  
DT 07-DEC-1998 (first entry)  
XX  
DE Erwinia amylovora hypersensitive response elicitor (HRE).  
XX  
KW Hypersensitive response elicitor; HRE; insect resistance;  
XX biological control; transgenic plant.  
XX  
OS Erwinia amylovora.  
XX  
PN W09837752-A1.  
XX  
PD 03-SEP-1998.  
XX  
PF 26-FEB-1998; 98WO-US03604.  
XX  
PR 28-FEB-1997; 97US-0039226.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX Wel Z, Zitter TA;  
XX  
DR WPI: 1998-495374/42.  
XX N-PSDB; AAW54607.  
XX  
PT Use of hypersensitive response elicitor polypeptide - for  
control of insects.  
PT application to plants or seeds or transgenic plants or seeds for the  
control of insects.

XX Disclosure; Page 9-10; 75pp; English.

CC This is the amino acid sequence of a 39 kDa, heat stable  
 CC hypersensitive response elicitor (HRE) of *Erwinia amylovora*. The  
 CC invention relates to the use of a HRE polypeptide or protein to  
 CC control insects on plants or plants grown from seed treated with HRE.  
 CC Also claimed is a method of insect control for plants that involves:  
 CC (a) providing a transgenic plant or seed transformed with a DNA  
 CC molecule (see AAV54606-09) encoding a HRE polypeptide or protein (see  
 CC AAV5862-67); and (b) growing the transgenic plants or transgenic  
 CC plants produced from the transgenic seeds to control insects. HRE  
 CC prevents direct insect damage to plants by feeding injury. It kills  
 CC insects close to plants, and interferes with insect larval feeding  
 CC on such plants. It also prevents insects from colonizing host  
 CC plants and releasing phytotoxins which result in disease damage to  
 CC plants.

CC Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 19; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGIGASTMGIISIGAGGNNGLGTSRONAGIGGNSALGIGGNNNDVYNOLAGLL 60  
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 DB 61 TGMAMMMMSMGGGGLMGGLGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
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 DB 121 TTSTNSPLDQALGINTSNDSTSGTSDTSDSSDPMOQLKMFSEIMQSLFGDGQDGT 180  
 QY 181 QGSSSGGKOPTGEONAYKRGVTDALSGIMNGLSQLLNGGLGGGOGGNACTGLDGSSTL 240  
 DB 181 QGSSSGGKOPTGEONAYKRGVTDALSGIMNGLSQLLNGGLGGGOGGNACTGLDGSSTL 240  
 QY 241 GKGGLQNLGSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNKKDRAMAKEI 300  
 DB 241 GKGGLQNLGSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNKKDRAMAKEI 300  
 QY 301 GGFMDQYEVFEGKPYOKRGPGQEVKTDDKSMKALSKPDDGMPASMEQFNKAGMIR 360  
 DB 301 GGFMDQYEVFEGKPYOKRGPGQEVKTDDKSMKALSKPDDGMPASMEQFNKAGMIR 360  
 QY 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNNALGRLGAA 403  
 DB 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNNALGRLGAA 403

RESULT 2  
 AAM62455  
 ID AAM62455 standard; Protein; 403 AA.

AC AAM62455;  
 XX 09-NOV-1998 (first entry)  
 DE *Erwinia amylovora* hypersensitive response elicitor (HRE).  
 XX *Erwinia amylovora*.  
 OS *Erwinia amylovora*.  
 XX WO9832844-A1.  
 PN 30-JUL-1998.  
 PD 27-JAN-1998; 98WO-US01507.  
 XX

PR 27-JAN-1997; 97US-0036048.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Beer SV, Qiu D, Wei Z;  
 XX  
 DR WPI, 1998-427940/36.  
 XX  
 DR N-PDB; AAV39973.  
 XX

PT Method for enhancing plant growth - comprises use of hypersensitive  
 PT response elicitor polypeptide or protein which may also effect, e.g.  
 PT increase in plant height or earlier germination seed  
 PS disclosure; Page 15-16; 110pp; English.

CC This is the deduced amino acid sequence of the 39 kDa, heat stable  
 CC hypersensitive response elicitor (HRE) of *Erwinia amylovora*. A  
 CC method of enhancing growth in plants comprises: (a) applying a HRE  
 CC polypeptide or protein in a non-infectious form to a plant or plant  
 CC seed under conditions effective to enhance growth of the plant or  
 CC plants grown from the seed, or (b) providing a transgenic plant or  
 CC plant seed transformed with a DNA molecule encoding a HRE  
 CC polypeptide or protein, and growing the transgenic plant or a plant  
 CC produced from the transgenic seed under conditions effective to  
 CC enhance plant growth. HRES (see AAM62454-59) or nucleic acids  
 CC encoding them (see AAV39972-75) can be used to increase plant growth.  
 CC The HRES may also result in increased plant height and yield, and  
 CC effect early germination and maturation of plant seed and early  
 CC coloration of fruit and plants. *E. amylovora* HRE can be applied  
 CC to tomato plants to enhance growth without causing disease in that  
 CC species; this bacterium is a pathogen of apple and pear but not  
 CC of tomato.

CC Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 19; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 181 QGSSSGGKOPTGEONAYKRGVTDALSGIMNGLSQLLNGGLGGGOGGNACTGLDGSSTL 240  
 QY 241 GKGGLQNLGSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNKKDRAMAKEI 300  
 DB 241 GKGGLQNLGSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNKKDRAMAKEI 300  
 QY 301 GGFMDQYEVFEGKPYOKRGPGQEVKTDDKSMKALSKPDDGMPASMEQFNKAGMIR 360  
 DB 301 GGFMDQYEVFEGKPYOKRGPGQEVKTDDKSMKALSKPDDGMPASMEQFNKAGMIR 360  
 QY 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNNALGRLGAA 403  
 DB 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNNALGRLGAA 403

RESULT 3  
 AAM61114  
 ID AAM61114 standard; Protein; 403 AA.  
 XX  
 AC AAM61114;

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XX 26-OCT-1998 (first entry)
XX Hypersensitive response elicitor protein (39 kDa).
DE Hypersensitive response elicitor; transgenic plant; seed;
KM pathogen resistance; disease resistance; crop protection.
XX Erwinia amylovora.
XX MO9824297-A1.
XX 11-JUN-1998.
XX 04-DEC-1997; 97MO-US22629.
XX 05-DEC-1996; 96DS-0033230.
XX (CORR ) CORNELL RES FOUND INC.
XX Beer SV, Qiu D, Wei Z;
XX WPI; 1998-332931/29.
XX N-PSDB; AAV36428.
XX Imparting pathogen resistance to plants - by applying a
XX hypersensitive response elicitor polypeptide to seeds
XX Disclosure; Page 18-20; 85pp; English.
XX This is the 39 kDa hypersensitive elicitor (HRE) protein of
XX Erwinia amylovora. It is heat stable at 100 degC for at least 10
XX min, has a pI of approximately 4.3, and contains substantially no
XX cysteine. The invention relates to methods of imparting no
XX hypersensitive response induced resistance to plants by treatment
XX of seeds. Isolated HRE proteins can be applied to seeds as a means
XX of imparting pathogen resistance to plants grown from the seeds.
XX Alternatively, bacteria containing the gene encoding the HRE can be
XX applied to the plant seeds, or transgenic plant seeds containing a
XX DNA molecule encoding an HRE polypeptide or protein are used. HRE
XX polypeptide sequences from Erwinia chrysanthemi, Erwinia amylovora,
XX Pseudomonas syringae, Pseudomonas solanacearum, Xanthomonas
XX campestris pv. glycines and Xanthomonas campestris pelargonii (see
XX AAW6113-18) are provided. The methods can impart pathogen
XX resistance without using agents which are harmful to the
XX environment or pathogenic to the plant seed being treated, or to
XX adjacent plants. E. amylovora causes disease in apple or pear
XX but not tomato. However, it elicits a hypersensitive response in
XX tomato. Thus, E. amylovora can be applied to tomato seeds to
XX impart pathogen resistance without causing diseases in plants of
XX that species.
XX
XX Sequence 403 AA:
XX
XX Query Match 100.0%; Score 2079; DB 19; Length 403;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-155;
XX Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 301 GGFMDQYPEVFGKRPQYOKPGCEVETKDDSKVAKALSRPDDGKMPASMEQFNKAKMIKR 360
DB 301 GGFMDQYPEVFGKRPQYOKPGCEVETKDDSKVAKALSRPDDGKMPASMEQFNKAKMIKR 360
OY 361 PMAGDTGNGNLQARAGAGSSSLGIDAMAGDAINNMALGKLGAA 403
DB 361 PMAGDTGNGNLQARAGAGSSSLGIDAMAGDAINNMALGKLGAA 403

RESULT 4
AAW87639
ID AAW87639 standard; Protein; 403 AA.
XX
XX AAW87639;
XX
XX 09-MAR-1999 (first entry)
XX
XX A hypersensitive response elicitor protein.
XX
XX Hypersensitive response elicitor protein; hairpin protein;
XX disease resistance; seed quality; insect control; corn borer;
XX Lepidoptera larvae; transgenic plant.
XX
XX Erwinia amylovora.
XX
XX MO9854214-A2.
XX
XX 03-DEC-1998.
XX
XX 28-MAY-1998; 98MO-US10874.
XX
XX 30-MAY-1997; 97US-0048109.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX (EDEN-) EDEN BIOSCIENCE CORP.
XX
XX Beer SV, Laby RJ, Wei Z;
XX
XX WPI; 1999-070210/06.
XX N-PSDB; AAV83989.
XX
XX New fragments of an Erwinia hypersensitive response elicitor protein
XX and related DNA - used to impart disease resistance to plants, to
XX increase their growth and to control insects
XX
XX Claim 4; Page 10-11; 94pp; English.
XX
XX The present sequence represents a hypersensitive response elicitor
XX protein (also called hairpin protein) that is able to elicit a
XX hypersensitive response in plants. The specification also describes
XX hypersensitive response elicitors from other pathogenic organisms.
XX The protein, in non-infectious form, is applied to plants to impart
XX disease resistance (to a wide range of viral, bacterial and fungal
XX pathogens), to improve growth (yield, quantity and quality of seeds,
XX to provide earlier germination etc.) and to control insects (e.g. corn
XX borers, Lepidoptera larvae etc.) The same results are provided by
XX transgenic plants expressing the protein.
XX
XX Sequence 403 AA:
XX
XX Query Match 100.0%; Score 2079; DB 20; Length 403;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-155;
XX Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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 DB 181 QGSSSGKOPTREBQNAKRYKGYVDALSLGMLNGLSQLLNGNGLGCGGCGNAGTGLDSSSL 240  
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 DB 241 GKGGLQNLGSPVDYQQLGNAVGTGIGMKAGIOALNDIGTRHSSTRSFYKNGDRAMAKEY 300  
 QY 301 GGFMDQYPEYFGKPOYOKGPGQEVKTDKSWAKALSRPDDGKMTPASMEQFNKAKGMKIR 360  
 DB 301 GGFMDQYPEYFGKPOYOKGPGQEVKTDKSWAKALSRPDDGKMTPASMEQFNKAKGMKIR 360  
 QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403  
 DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403

# RESULT 5 AAY71093

ID AAY71093 standard; Protein: 403 AA.

AC AAY71093;

DT 08-SEP-2000 (first entry)

DE Erwilia amylovora hypersensitive response elicitor #1.

KW Hypersensitive response elicitor; environmental stress resistance;  
 plant.

OS Erwilia amylovora.

PN W0200028055-A2.

PD 18-MAY-2000.

PF 04-NOV-1999; 99WO-US26039.

PR 05-NOV-1998; 98US-0107243.

PA (EDEN-) EDEN BIOSCIENCE CORP.

PI Wei Z, Schading RL;

DR WPI; 2000-376566/32.

DR N-PSDB; AAD00668.

PT Application of a hypersensitive response elicitor protein to plants to  
 impart stress resistance

PS Disclosure; Page 7-8; 84pp; English.

CC The patent discloses a method to impart stress resistance to plants by  
 applying a hypersensitive response elicitor in a non-infectious form to

CC a plant or seed. The present sequence is a hypersensitive

CC response elicitor protein from Erwilia amylovora. It is

CC is used to impart stress resistance to plants.

XX Sequence 403 AA;

QY Query Match 100.0%; Score 2079; DB 21; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-153;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSINTSGIGASTMQISIGAGGNNGLGTSRQNAGLGAGSALGIGGNGNDTVNQLAGL 60  
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 QY 181 QGSSSGKOPTREBQNAKRYKGYVDALSLGMLNGLSQLLNGNGLGCGGCGNAGTGLDSSSL 240  
 DB 181 QGSSSGKOPTREBQNAKRYKGYVDALSLGMLNGLSQLLNGNGLGCGGCGNAGTGLDSSSL 240  
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 QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403  
 DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403

# RESULT 6 AAY84854

ID AAY84854 standard; Protein: 403 AA.

AC AAY84854;

DT 08-AUG-2000 (first entry)

DE A hypersensitive response elicitor protein.

KW Hypersensitive response; insect control; disease resistance;  
 hypersensitive response elicitor; plant growth; vegetable; crop;  
 ornamental plant.

OS Erwilia amylovora.

PN W0200020452-A2.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23181.

PR 05-OCT-1998; 98US-0103050.

PA (EDEN-) EDEN BIOSCIENCE CORP.

PI Wei Z, Fan H, Niggemeyer JL;

FT key

FT location/Qualifiers

FT 169..403

FT /note- "claimed under claim 5"

FT 210..403

FT /note- "claimed under claim 5"

FT 267..403

FT /note- "claimed under claim 5"

FT 343..403

FT /note- "claimed under claim 5"

FT 105..179

FT /note- "claimed under claim 7"

FT 121..150

FT /note- "claimed under claim 7"

FT 137..166

FT /note- "claimed under claim 7"

FT 137..156

FT /note- "claimed under claim 7"XX

XX WPI: 2000-303745/26.  
 DR N-PSDB: AAL14938.  
 XX Hypersensitive response elicitor polypeptides useful for imparting  
 PT enhanced growth, disease resistance and insect resistance to plants,  
 PT especially vegetables and ornamental flowers -  
 XX  
 PS Claim 4; Page 8-10; 100pp; English.

CC The present sequence represents a hypersensitive response elicitor  
 CC polypeptide. The specification describes hypersensitive response  
 CC elicitor polypeptide fragments, which do not elicit a hypersensitive  
 CC response. Instead, the proteins impart disease resistance to plants,  
 CC enhance plant growth, and/or control insects. The polypeptide  
 CC fragments may be used to these properties to plants. The plants which  
 CC may be treated in this way include vegetables, crops and ornamental  
 CC plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower,  
 CC peanut, corn, potato, sweet potato, bean, pea, chickory, lettuce,  
 CC endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower,  
 CC broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery,  
 CC carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon,  
 CC citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco,  
 CC tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia,  
 CC petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia.

XX Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 21; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGIGASTMQISIGAGGNNGLGTSRONAGLGSNALSALGIGGNDYVNOAGL 60  
 DB 1 MSINTSGIGASTMQISIGAGGNNGLGTSRONAGLGSNALSALGIGGNDYVNOAGL 60

QY 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120

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 DB 181 QGSSSGKOPTBEQONAYKRGVTDALSGLMNGLSQLLNGGGLGGGCGNAGTGLDSSL 240

QY 241 GKGGLQNLSPVYQOOLGNVGTGIGMKAGIOALNDIGTHRSSTSFVAKGDRAMAKEI 300  
 DB 241 GKGGLQNLSPVYQOOLGNVGTGIGMKAGIOALNDIGTHRSSTSFVAKGDRAMAKEI 300

QY 301 GGFMDQYPEVFGKPOYOKGPGOEKTDKSMARALSKPDDDGMTPAEMGFNRAKMIKR 360  
 DB 301 GGFMDQYPEVFGKPOYOKGPGOEKTDKSMARALSKPDDDGMTPAEMGFNRAKMIKR 360

QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAAGLKGAA 403  
 DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAAGLKGAA 403

RESULT 7  
 ID AAE06710 standard; Protein; 403 AA.  
 XX  
 AC AAE06710;

DT 16-OCT-2001 (first entry)  
 XX  
 DE Erwinia amylovora hypersensitive response elicitor protein.  
 XX  
 KW Hypersensitive response elicitor; oomycete; transgenic plant; infection;  
 KW gene therapy; crop loss; antifungal.

XX  
 OS Erwinia amylovora.  
 XX  
 PN NO200155347-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001MO-US02579.  
 XX  
 PR 26-JAN-2000; 2000US-0178565.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Beer SV, Bauer DW;  
 XX  
 DR WPI: 2001-486791/53.  
 DR N-PSDB: AAD12806.

XX New chimeric gene, useful for controlling plant-pathogenic fungi and  
 PT producing oomycete-resistant transgenic plants, comprises first DNA  
 PT encoding hypersensitive response elicitor, promoter and regulatory  
 region -  
 XX  
 PS Claim 9; Page 13-14; 72pp; English.

CC The invention relates to a chimeric gene that includes a first DNA  
 CC molecule encoding a hypersensitive response elicitor protein or  
 CC polypeptide, promoter operably linked 5' to the first DNA molecule  
 CC to induce transcription of the first DNA molecule in response to  
 CC activation of the promoter by an oomycete and a 3' regulatory region  
 CC operably linked to the first DNA molecule. The invention also relates  
 CC to a transgenic plant resistant to disease resulting from oomycete  
 CC infection, the transgenic plant including the chimeric gene, wherein  
 CC the promoter induces transcription of the first DNA molecule in  
 CC response to infection of the plant by an oomycete. The chimeric gene  
 CC is used in gene therapy. The chimeric gene is useful as an effective  
 CC and safe means of controlling plant-pathogenic fungi, particularly  
 CC oomycetes, which are responsible for major crop loss and is also useful  
 CC for producing transgenic plants of the invention. The present sequence  
 CC is Erwinia amylovora hypersensitive response elicitor protein.

XX Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 22; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGIGASTMQISIGAGGNNGLGTSRONAGLGSNALSALGIGGNDYVNOAGL 60  
 DB 1 MSINTSGIGASTMQISIGAGGNNGLGTSRONAGLGSNALSALGIGGNDYVNOAGL 60

QY 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120

QY 121 TTSTNSPDLQALGINTSONDSTSGTSTSDSPDMOQLKMFSEIMOSLFGDGDGT 180  
 DB 121 TTSTNSPDLQALGINTSONDSTSGTSTSDSPDMOQLKMFSEIMOSLFGDGDGT 180

QY 181 QGSSSGKOPTBEQONAYKRGVTDALSGLMNGLSQLLNGGGLGGGCGNAGTGLDSSL 240  
 DB 181 QGSSSGKOPTBEQONAYKRGVTDALSGLMNGLSQLLNGGGLGGGCGNAGTGLDSSL 240

QY 241 GKGGLQNLSPVYQOOLGNVGTGIGMKAGIOALNDIGTHRSSTSFVAKGDRAMAKEI 300  
 DB 241 GKGGLQNLSPVYQOOLGNVGTGIGMKAGIOALNDIGTHRSSTSFVAKGDRAMAKEI 300

QY 301 GGFMDQYPEVFGKPOYOKGPGOEKTDKSMARALSKPDDDGMTPAEMGFNRAKMIKR 360  
 DB 301 GGFMDQYPEVFGKPOYOKGPGOEKTDKSMARALSKPDDDGMTPAEMGFNRAKMIKR 360

QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAAGLKGAA 403  
 DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAAGLKGAA 403

Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINMMALGKLGAA 403

RESULT 8  
ID ABB09225 standard; Protein: 403 AA.  
XX ABB09225;  
XX 08-JUL-2002 (first entry)  
XX  
XX Erwinia amylovora hypersensitive response elicitor SEQ ID NO:3.  
XX  
XX Hypersensitive response elicitor; fruit; vegetable; plant; desiccation;  
XX postharvest disease.  
XX  
XX Erwinia amylovora.  
XX OS  
XX WO200180639-A2.  
XX PN  
XX 01-NOV-2001.  
XX PD  
XX 17-APR-2001; 2001WO-US12468.  
XX PF  
XX 19-APR-2000; 2000US-198359P.  
XX PR  
XX (EDEN-) EDEN BIOSCIENCE CORP.  
XX PA  
XX Wei Z, Qiu D, Remick D;  
XX PI  
XX WPI: 2002-041357/05.  
XX DR N-PSDB; ABL51710.  
XX DR  
XX Inhibiting post harvest disease (caused by Penicillium, Botrytis,  
XX Phytophthora, or Erwinia) or desiccation and enhancing the longevity in  
XX a fruits or vegetables, using hypersensitive response elicitor proteins  
XX or nucleic acids -  
XX  
XX Example; Page 9-10; 72pp; English.  
XX  
XX The present invention describes methods for inhibiting post harvest  
XX disease or desiccation and enhancing the longevity in a fruits or  
XX vegetables, using hypersensitive response elicitor proteins or  
XX polypeptides or nucleic acids (I) derived from pathogens (e.g. Erwinia  
XX amylovora, E. stewartii, E. chrysanthemi, E. carotovora, Xanthomonas,  
XX Pseudomonas syringae, P. solanacearum, Phytophthora, and Clavibacter).  
XX (I) has bactericidal activity, and can be used in gene therapy. The  
XX method can be used for inhibiting post harvest disease (caused by  
XX Penicillium, Botrytis, Phytophthora, or Erwinia) or desiccation and  
XX enhancing the longevity in a fruits or vegetables. The method enables  
XX growers, warehouse packers, shippers and suppliers to process, handle  
XX and store fruit and vegetables with reduced losses caused by post harvest  
XX disease and desiccation, therefore reducing costs to the consumer and  
XX improving quality. The present sequence represents a hypersensitive  
XX response elicitor protein given in the exemplification of the present  
XX invention.  
XX  
XX Sequence 403 AA:  
SQ  
Query Match 100.0%; Score 2079; DB 23; Length 403;  
Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLGLGASTWQISIGGAGGNGLLGTSRONAGLGSNSALGIGGQNDVTYNQLAGLL 60  
DB 1 MSLSLGLGASTWQISIGGAGGNGLLGTSRONAGLGSNSALGIGGQNDVTYNQLAGLL 60  
QY 1 TGNHMMMSMMGGGGLMGGGIGGGIGGNGIGGGGIGGEGSNALNMLGSLNLTLSKGGNN 120  
DB 1 TGNHMMMSMMGGGGLMGGGIGGGIGGNGIGGGGIGGEGSNALNMLGSLNLTLSKGGNN 120  
QY 61 TGNHMMMSMMGGGGLMGGGIGGGIGGNGIGGGGIGGEGSNALNMLGSLNLTLSKGGNN 120  
DB 61 TGNHMMMSMMGGGGLMGGGIGGGIGGNGIGGGGIGGEGSNALNMLGSLNLTLSKGGNN 120  
QY 121 TTSTTNSPLDQALGINSTQNDSTSGTDSSTSDSPMOQLKMFSEIMOSLFGDGQDGT 180  
DB 121 TTSTTNSPLDQALGINSTQNDSTSGTDSSTSDSPMOQLKMFSEIMOSLFGDGQDGT 180

Db 121 TTSTTNSPLDQALGINSTQNDSTSGTDSSTSDSPMOQLKMFSEIMOSLFGDGQDGT 180

QY 181 QGSSSGGKQPTGEGQNAKKGVTDALSGIMNGSLGSLGNGSLGGGQGNAGTGLDSSL 240  
DB 181 QGSSSGGKQPTGEGQNAKKGVTDALSGIMNGSLGSLGNGSLGGGQGNAGTGLDSSL 240  
QY 241 GKGGLQNLGSPVDYQOGLNAVGTGIGMKAGIQALNDIGTHRHSSTRSFVNNGDPAKKEI 300  
DB 241 GKGGLQNLGSPVDYQOGLNAVGTGIGMKAGIQALNDIGTHRHSSTRSFVNNGDPAKKEI 300  
QY 301 GQFMDQYPEVFGKPOYQKRGQEVKTDKSNKALSRPDDGKTPASKEQPNKAKMKIR 360  
DB 301 GQFMDQYPEVFGKPOYQKRGQEVKTDKSNKALSRPDDGKTPASKEQPNKAKMKIR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINMMALGKLGAA 403  
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINMMALGKLGAA 403

RESULT 9  
ID AAE18295 standard; Protein: 403 AA.  
XX AAE18295;  
XX AAE18295;  
XX 07-MAY-2002 (first entry)  
XX DT  
XX Erwinia amylovora hypersensitive response elicitor (HRE) #1.  
XX DE  
XX Hypersensitive response elicitor; HRE; transgenic plant; plant growth;  
XX stress tolerance; disease tolerance; modified flower colour;  
XX insect resistance; herbicide resistance; male sterility.  
XX OS  
XX Erwinia amylovora.  
XX PN  
XX WO200195724-A2.  
XX PD  
XX 20-DEC-2001.  
XX PF  
XX 13-JUN-2001; 2001WO-US18955.  
XX PR  
XX 15-JUN-2000; 2000US-211585P.  
XX PA  
XX (EDEN-) EDEN BIOSCIENCE CORP.  
XX PI  
XX Wei Z, Derocher J;  
XX N-PSDB; AAD29124.  
XX WPI: 2002-130707/17.  
XX DR  
XX Improving effectiveness of transgenic plants by topical application of  
XX a hypersensitive response elicitor protein to the transgenic plant or  
XX by incorporating into the plant a transgene encoding the protein -  
XX Disclosure; Page 10-11; 86pp; English.  
XX  
XX The invention relates to methods of improving the effectiveness of  
XX transgenic plants which involves either topical application of a  
XX hypersensitive response elicitor (HRE) protein to the transgenic plant  
XX or incorporating into the transgenic plant a transgene encoding HRE.  
XX HRE sequence is used for improving the effectiveness of transgenic  
XX plants by maximising the benefit of transgenic traits associated with  
XX a deleterious effect on growth, stress tolerance, disease or insect  
XX resistance, enhanced growth, herbicide resistance, male sterility,  
XX modified flower colour and biochemically modified plant product in  
XX the transgenic plants or overcoming the deleterious effects. The  
XX present sequence is Erwinia amylovora HRE protein.  
XX  
XX Sequence 403 AA:  
SQ  
Query Match 100.0%; Score 2079; DB 23; Length 403;  
Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGLASTMOWISTGAGAGNNGILGTSRONAGLGSNALSALGAGGNDNDYVQIAGL 60  
 DB 1 MSINTSGLASTMOWISTGAGAGNNGILGTSRONAGLGSNALSALGAGGNDNDYVQIAGL 60  
 QY 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 QY 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSPDMOOLKMFSEIMOSLFGDGODGT 180  
 DB 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSPDMOOLKMFSEIMOSLFGDGODGT 180  
 QY 181 QGSSSGGKOPTEBEQONAKKGYTDALSGLMGNGLSQLLNGGGLGGGGGAGNAGTGLDSSSL 240  
 DB 181 QGSSSGGKOPTEBEQONAKKGYTDALSGLMGNGLSQLLNGGGLGGGGGAGNAGTGLDSSSL 240  
 QY 241 GGGKGLQNLGSPVDYQOLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFYVKKGRAMAKET 300  
 DB 241 GGGKGLQNLGSPVDYQOLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFYVKKGRAMAKET 300  
 QY 301 GGFMDQYPEVFGKPOYOKGPGOEKVTDDKSMARALSKPDDGKTPASMEQFNKAKGMIKR 360  
 DB 301 GGFMDQYPEVFGKPOYOKGPGOEKVTDDKSMARALSKPDDGKTPASMEQFNKAKGMIKR 360  
 QY 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
 DB 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNMALGKLGAA 403

RESULT 10  
 AAE16447  
 ID AAE16447 standard; Protein; 403 AA.  
 AC AAE16447;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE E. amylovora hypersensitive response elicitor protein #1.  
 XX  
 KW Hypersensitive response elicitor protein; plant growth; fruit coloration;  
 KW disease resistance; stress resistance; phytoalexin; insect infection;  
 KW plant maturation.  
 XX  
 OS Erwinia amylovora.  
 OS  
 FH Key Location/Qualifiers  
 FT Domain 32..74  
 FT /label= Hypersensitive\_response\_eliciting\_domain\_1  
 FT Region 32..57  
 FT /label= Acidic\_unit  
 FT Region 57..74  
 FT /label= Alpha\_helix  
 FT Domain 130..180  
 FT /label= Hypersensitive\_response\_eliciting\_domain\_2  
 FT Region 130..157  
 FT /label= Acidic\_unit  
 FT Region 157..180  
 FT /label= Alpha\_helix  
 FT  
 PN WO200196501-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 12-JUN-2001; 2001WO-US18820.  
 XX  
 PR 16-JUN-2000; 2000US-212211P.  
 XX  
 PA (EDEN-) EDEN BIOSCIENCE CORP.  
 XX  
 PI Fan H, Wei Z;  
 XX  
 DR WPI; 2002-122282/16.

DR N-PSDB; AAD27015.  
 XX  
 PT New hypersensitive response elicitor proteins comprising spaced apart  
 PT domains having an acidic portion linked to an alpha-helix, useful for  
 PT imparting disease or stress resistance, controlling insects or  
 PT enhancing plant growth -  
 XX  
 PS Disclosure; Page 9-10; 9pp; English.  
 PS  
 XX  
 CC The patent discloses hypersensitive response elicitor proteins and  
 CC nucleotides encoding such proteins. Hypersensitive response elicitor  
 CC proteins comprise an isolated pair or more of spaced apart domains,  
 CC each comprising an acidic portion linked to an alpha-helix and capable  
 CC of eliciting a hypersensitive response in plants. Sequences of the  
 CC invention are used to impart disease resistance to plants, to enhance  
 CC plant growth, to control insects and/or to impart stress resistance  
 CC to plants which includes resistance to environmental stresses such as  
 CC climate, air pollution, chemical and nutritional stress. The method of  
 CC imparting disease resistance has the potential for treating previously  
 CC untreatable diseases, treating diseases systemically and avoiding the  
 CC use of infectious agents or environmentally harmful materials. Hyper-  
 CC sensitive response elicitor sequences are used to enhance plant growth  
 CC which encompasses greater yield, increased in quantity of seeds produced,  
 CC percentage of seeds germinated, plant size and biomass, bigger fruits,  
 CC earlier fruit coloration and plant maturation. They are also used for  
 CC insect control which encompasses preventing direct insect damage to  
 CC plant by feeding injury, interfering with insect larval feeding on the  
 CC plants, preventing insects from colonizing host plants and releasing  
 CC phytochemicals. Sequences of the invention also prevent subsequent disease  
 CC damage to plants resulting from insect infection. The present sequence  
 CC is Erwinia amylovora hypersensitive response elicitor protein.  
 XX  
 SO Sequence 403 AA;  
 XX

Query Match 100.0%; Score 2079; DB 23; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGLASTMOWISTGAGAGNNGILGTSRONAGLGSNALSALGAGGNDNDYVQIAGL 60  
 DB 1 MSINTSGLASTMOWISTGAGAGNNGILGTSRONAGLGSNALSALGAGGNDNDYVQIAGL 60  
 QY 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 TGMAMMAMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 QY 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSPDMOOLKMFSEIMOSLFGDGODGT 180  
 DB 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSPDMOOLKMFSEIMOSLFGDGODGT 180  
 QY 181 QGSSSGGKOPTEBEQONAKKGYTDALSGLMGNGLSQLLNGGGLGGGGGAGNAGTGLDSSSL 240  
 DB 181 QGSSSGGKOPTEBEQONAKKGYTDALSGLMGNGLSQLLNGGGLGGGGGAGNAGTGLDSSSL 240  
 QY 241 GGGKGLQNLGSPVDYQOLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFYVKKGRAMAKET 300  
 DB 241 GGGKGLQNLGSPVDYQOLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFYVKKGRAMAKET 300  
 QY 301 GGFMDQYPEVFGKPOYOKGPGOEKVTDDKSMARALSKPDDGKTPASMEQFNKAKGMIKR 360  
 DB 301 GGFMDQYPEVFGKPOYOKGPGOEKVTDDKSMARALSKPDDGKTPASMEQFNKAKGMIKR 360  
 QY 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
 DB 361 PMAGDTGNGNLOARGAGSSSLGIDAMAGDAINNMALGKLGAA 403

RESULT 11  
 AAW06598  
 ID AAW06598 standard; Protein; 385 AA.  
 AC AAW06598;  
 XX

DT 30-MAR-1997 (first entry)  
 XX Hypersensitive response elicitor protein.  
 DE  
 XX  
 KM Hypersensitive response; elicitor; Erwinia amylovora; plant;  
 KM disease-resistance; Escherichia coli; infiltration; virus;  
 KM bacterium; fungus; pathogen; biological control agent.  
 OS  
 XX Erwinia amylovora.  
 XX  
 PN K09639802-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 05-JUN-1996; 96WO-US08819.  
 XX  
 PR 07-JUN-1995; 95US-0475775.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Beer SV, Wei Z;  
 XX  
 DR WPI; 1997-051614/05.  
 DR N-PSDB; AAT9314.  
 XX  
 XX Imparting pathogen resistance to plants - with hypersensitive  
 PT response elicitor polypeptide or protein  
 XX  
 PS Claim 7; Page 46-47; 69pp; English.  
 XX  
 CC This sequence represents a hypersensitive response elicitor from  
 CC Erwinia amylovora, with a mol.wt. of 37,000. The elicitor has a pI  
 CC of 4.3, thermostability at 100 deg C for at least 10 min, and  
 CC contains no cysteine. The elicitor may be used in a new method for  
 CC imparting pathogen resistance to plants, by application of the  
 CC elicitor in a non-infectious form to plant cells, by spraying,  
 CC injection, leaf abrasion, or plant infection with recombinant  
 CC bacteria (non-infectious to the host plant, e.g. Escherichia coli)  
 CC expressing the elicitor as a biological control agent, to allow  
 CC recombinant protein infiltration into the plant. The method  
 CC confers virus, bacterium or fungus disease-resistance on crops and  
 CC ornamental plants.  
 CC  
 XX  
 SQ Sequence 385 AA;  
 Query Match 92.7%; Score 1928; DB 18; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-143;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 361 PMAGDTGNGNMQ 372  
 |||||||||  
 DB 361 PMAGDTGNGNMQ 372  
 RESULT 12  
 ID AAR45751 standard; Protein; 385 AA.  
 XX  
 AC AAR45751;  
 XX  
 DT 11-JUL-1994 (first entry).  
 XX  
 DE Erwinia amylovora harpin.  
 XX  
 KM Harpin; hypersensitive response elicitor; HR-elicitor; fire blight;  
 KM Rosaceae; apple; pear; phytopathogenic bacteria; defence reaction;  
 KM hypersensitive reaction and pathogenicity; hrpN; gene cluster; ds.  
 XX  
 OS Erwinia amylovora.  
 XX  
 FH Key location/Qualifiers  
 FT MISC-difference 372  
 FT MISC-difference 372 /note- "corresponds to CAG codon"  
 FT MISC-difference 373 /note- "corresponds to CAC codon"  
 XX  
 FN K09401546-A.  
 XX  
 PD 20-JAN-1994.  
 XX  
 PF 30-JUN-1993; 93WO-US06243.  
 XX  
 PR 01-JUL-1992; 92US-0907935.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Bauer DW, Beer SV, Collmer A, He S, Lady R, Wei Z;  
 XX  
 DR WPI; 1994-035054/04.  
 DR N-PSDB; AAO55751.  
 XX  
 XX Hypersensitive response elicitor protein derived from Erwinia  
 PT amylovora - and DNA encoding it, useful for developing harpin  
 PT inhibitors to prevent e.g. fire blight of fruit  
 XX  
 PS Claim 6; Page 27-28; 47pp; English.  
 XX  
 CC The hrpN gene was isolated from E. amylovora using a 48-fold  
 CC degenerate oligonucleotide probe corresponding to amino acids 9-15  
 CC at the N-terminus of harpin. The 44kD protein encoded by the hrpN  
 CC gene is a hypersensitive response elicitor protein. The harpin is  
 CC thought to be an archetype for HR elicitors from phytopathogenic  
 CC bacteria.  
 CC  
 XX  
 SQ Sequence 385 AA;  
 Query Match 92.0%; Score 1913; DB 15; Length 385;  
 Best Local Similarity 99.5%; Pred. No. 3.3e-142;  
 Matches 369; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



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OY 181 QGSSSGKQPTREGONAYKKVTYDALSGLMNGLSQLLGNGLGGGCGGAGTGLDGSSTL 240
DB 181 QGSSSGKQPTREGONAYKKVTYDALSGLMNGLSQLLGNGLGGGCGGAGTGLDGSSTL 240
OY 241 GKGGLQNTSGPVDYQOLGNVGTGIGMAGAGIOLNDIGTHRSSSTRSFVNRKDDRAMAKKI 300
DB 241 GKGGLQNTSGPVDYQOLGNVGTGIGMAGAGIOLNDIGTHRSSSTRSFVNRKDDRAMAKKI 300
OY 301 GGFMDQYEFVEFGKPYOKGPGQEVETDDKSNPAKALSKPDDOGMTFASMEQFNKAGMKIR 360
DB 301 GGFMDQYEFVEFGKPYOKGPGQEVETDDKSNPAKALSKPDDOGMTFASMEQFNKAGMKIR 360
OY 361 PMAGDTGNGNTL 371
DB 361 PMAGDTGNGNTL 371

RESULT 13
AAM06597
ID AAM06597 standard; Protein; 338 AA.
AC AAM06597;
DE 30-MAR-1997 (first entry)
XX Hypersensitive response elicitor protein.
DE Hypersensitive response elicitor protein.
KW Hypersensitive response; elicitor; Erwinia chrysanthemi; plant;
KW disease-resistance; Escherichia coli; infiltration; virus;
KW bacterium; fungus; pathogen; biological control agent.
XX Erwinia chrysanthemi.
XX MO9639802-A1.
XX 19-DEC-1996.
XX 05-JUN-1996; 96WO-US08819.
XX 07-JUN-1995; 95US-0475775.
XX (CORR ) CORNELL RES FOUND INC.
XX Beer SV, Wei Z;
XX MPI; 1997-051614/05.
XX N-PSDB; AAT49313.
XX Imparting pathogen resistance to plants - with hypersensitive
XX response elicitor polypeptide or protein
XX Claim 4; Page 44; 69pp; English.
XX This sequence represents a hypersensitive response elicitor from
XX Erwinia chrysanthemi, with a mol.wt. of 34,000. The elicitor is
XX thermostable, has a glycine content of over 16%, and has no cysteine.
XX The elicitor may be used in a new method for imparting pathogen
XX resistance to plants, by application of the elicitor in a non-
XX infectious form to plant cells, by spraying, injection, leaf
XX abrasion, or plant infection with recombinant bacteria (non-
XX infectious to the host plant, e.g. Escherichia coli) expressing the
XX elicitor as a biological control agent, to allow recombinant
XX protein infiltration into the plant. The method confers virus,
XX bacterium or fungus disease-resistance on crops and ornamental
XX plants.
XX Sequence 338 AA;
XX Query Match 34.6%; Score 718.5; DB 18; Length 338;
XX Best Local Similarity 42.8%; Pied. No. 18e-48;
XX Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;
OY 13 MOISI-GGAGGNGGLGTSRONAGLGG-NSA--LGLGGGNGNDVFNQLAGLLTGMMMM 67

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DB 1 MOTTIAHIGGDLGVSGLGAQ--GLKGLNSAASLSSSVYDKLSSTIDKTLFALTSMA---- 55
OY 68 SMAGGGGLGAGGGLGAGGGLGAGGGLGAGGGLGAGGGLGAGGGLGAGGGLGAGGGLGAGGGL 127
DB 56 -----FGALAGGGLGAS-SKGLMSNQLGQSGFN-----CAOGASNLISVPR- 96
OY 128 PLDQALGINSTSGNDSTSGTSTSDSPMQQLMFPEIMQSLFG-----DGCG 179
DB 97 -----SGDALS-----MFDAUDDLDGHDPTVKLNQSNQ 128
OY 180 TQSSSGKQPTREGONAYKKVTYDALSGLMNGLSQLLGNGLGGGCGGAGTGLDGSSTL 239
DB 129 LANSMLNASQMTGNNNAFGSVNNALSLILGGLGQSM-----SGPSQS 174
OY 240 LGKGLQNTSGPVDYQOLGNVGTGIGMAGAGIOLNDIGTHRSSSTRSFVNRKDDRAMAKE 299
DB 175 LGAGGLQNTSGPVDYQOLGNVGTGIGMAGAGIOLNDIGTHRSSSTRSFVNRKDDRAMAKE 234
OY 300 IGGFMDQYEFVEFGKPYOKGPGQEVETDDKSNPAKALSKPDDOGMTFASMEQFNKAGMKIR 359
DB 235 IGGFMDQYEFVEFGKPYOKGPGQEVETDDKSNPAKALSKPDDOGMTFASMEQFNKAGMKIR 294
OY 360 RPMAGDTGNGNTLQARGAGSSILGIDAMAGDAINNALKLGAA 403
DB 295 SAVAGDTGNTNMLRGAGGAGSLGIDAAVYCDRIANNSLGRKLANA 338

RESULT 14
AAM87638
ID AAM87638 standard; Protein; 338 AA.
AC AAM87638;
DE 09-MAR-1999 (first entry)
XX A hypersensitive response elicitor protein.
DE A hypersensitive response elicitor protein.
KW Hypersensitive response elicitor protein; hairpin protein;
KW disease resistance; seed quality; insect control; corn borer;
KW Lepidoptera larvae; transgenic plant.
XX Erwinia chrysanthemi.
XX OS
XX PN MO9854214-A2.
XX PD 03-DEC-1998.
XX PF 28-MAY-1998; 98WO-US10874.
XX PR 30-MAY-1997; 97US-0048109.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PA (EDEN-) EDEN BIOSCIENCE CORP.
XX PI Beer SV, Laby RJ, Wei Z;
XX DR MPI; 1999-070210/06.
XX DR N-PSDB; AAV83988.
XX PT New fragments of an Erwinia hypersensitive response elicitor protein
XX and related DNA - used to impart disease resistance to plants, to
XX increase their growth and to control insects
XX Disclosure; Page 7-8; 94pp; English.
XX The present sequence represents a hypersensitive response elicitor
XX protein (also called hairpin protein) that is able to elicit a
XX hypersensitive response in plants. The specification also describes
XX hypersensitive response elicitors from other pathogenic organisms.
XX The protein, in non-infectious form, is applied to plants to impart
XX disease resistance (to a wide range of viral, bacterial and fungal
XX pathogens), to improve growth (yield, quantity and quality of seeds,

```

CC to provide earlier germination etc.) and to control insects (e.g. corn  
CC borers, Lepidoptera larvae etc.) The same results are provided by  
CC transgenic plants expressing the protein.

XX Sequence 338 AA:

Query Match 34.6%; Score 718.5; DB 20; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.8e-48;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

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QY 13 MQIST-GGAGNNGLGTSRQNLGG-NSA---LGIGGNQNDYVNLGLTGMNMM 67
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 1 MQITRAHIGDGLGVSGIGAQ--GLKGLNSAASSLGSSVDKLSSTIDKLSALTSMV--- 55
QY 68 SMWGGGGLMGGLGGGIGNGLGSSGGLBELSNALNDMLGSLNTLGSKGGNNTTSTNS 127
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 56 -----FGALAQGLGAS-SKGLGMSNQLGSGFNG-----GAQASNLISVPK- 96
QY 128 PLDOALGINSTSONDSTSGTSDSDPMQQLKMFSEIMQSLFG-----DGQDG 179
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 97 -----SGDALSL-----KMFDAADDLGHDTVTTLTNQSNQ 128
QY 180 TQSSSSGCKOPTGEONAYKKVTDALSGIMNGLSQLLGNGLGGGQGGNAGTGLDSS 239
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 129 LANSMLNASQMTQGNNAFSGSVNNAISLILGNGLGSM-----SGFQPS 174
QY 240 LGGKGLONTSGPYDYOOLGNVGTGIGMKAGIQLANDIGHRHSSTRSFYKGDRAKAE 299
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 175 LGAGGLDGLSGAGAFNOLGNALIGVGNALSLSVSTHVGNHNFYDKEDRGMAKE 234
QY 300 IGFMDQYPEVFVKPOYOKPGQEVKTDKSNKALSKPDDDMTPASMEQFNKAKMIR 359
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 235 IGFMDQYPEIFKPEYOKDGMSSPKTDDKSNKALSKPDDDMTPASMDKFKQAMGMIK 294
QY 360 RPAAGTGNKNTLQARAGSSSLGIDMAMAGDAINNNAIGLGA 403
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 295 SAVAGDTGNTNMLRGAGASLIGIDAAYVGDKIANNISLKIANA 338

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RESULT 15

AAW82407 standard; Protein; 338 AA.

AC AAW82407;

DT 23-FEB-1999 (first entry)

DE E. chrysanthemi hrpN-Ech protein.

KM Hypersensitive response elicitor protein; hrpN-Ech; pathogen resistance;  
KM plant; transformation; pathogen-inducible promoter.

OS *Erwinia chrysanthemi*.

PN US5850015-A.

PD 15-DEC-1998.

PF 07-JUN-1995; 95US-0484358.

PR 07-JUN-1995; 95US-0484358.

PA (CORR ) CORNELL RES FOUND INC.

PI Bauer D, Collmer A;

DR WPI; 1999-069852/06.

DR N-PSDB; AAV73494, AAV73507.

PT DNA encoding *Erwinia chrysanthemi* hypersensitive response protein  
hrpN - useful for imparting pathogen resistance to plants

PS Claim 2; Column 29-30; 27p; English.

XX This sequence represents a novel *Erwinia chrysanthemi* protein, hrpN-Ech,  
CC that elicits a hypersensitive response in plants. The encoding DNA can be  
CC used for imparting pathogen resistance to plants, by transforming a  
CC plant with a vector containing the DNA and a pathogen-inducible promoter.

XX Sequence 338 AA:

Query Match 34.6%; Score 718.5; DB 20; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.8e-48;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

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QY 13 MQIST-GGAGNNGLGTSRQNLGG-NSA---LGIGGNQNDYVNLGLTGMNMM 67
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Db 1 MQITRAHIGDGLGVSGIGAQ--GLKGLNSAASSLGSSVDKLSSTIDKLSALTSMV--- 55
QY 68 SMWGGGGLMGGLGGGIGNGLGSSGGLBELSNALNDMLGSLNTLGSKGGNNTTSTNS 127
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 56 -----FGALAQGLGAS-SKGLGMSNQLGSGFNG-----GAQASNLISVPK- 96
QY 128 PLDOALGINSTSONDSTSGTSDSDPMQQLKMFSEIMQSLFG-----DGQDG 179
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 97 -----SGDALSL-----KMFDAADDLGHDTVTTLTNQSNQ 128
QY 180 TQSSSSGCKOPTGEONAYKKVTDALSGIMNGLSQLLGNGLGGGQGGNAGTGLDSS 239
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 129 LANSMLNASQMTQGNNAFSGSVNNAISLILGNGLGSM-----SGFQPS 174
QY 240 LGGKGLONTSGPYDYOOLGNVGTGIGMKAGIQLANDIGHRHSSTRSFYKGDRAKAE 299
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 175 LGAGGLDGLSGAGAFNOLGNALIGVGNALSLSVSTHVGNHNFYDKEDRGMAKE 234
QY 300 IGFMDQYPEVFVKPOYOKPGQEVKTDKSNKALSKPDDDMTPASMEQFNKAKMIR 359
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 235 IGFMDQYPEIFKPEYOKDGMSSPKTDDKSNKALSKPDDDMTPASMDKFKQAMGMIK 294
QY 360 RPAAGTGNKNTLQARAGSSSLGIDMAMAGDAINNNAIGLGA 403
   |||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 295 SAVAGDTGNTNMLRGAGASLIGIDAAYVGDKIANNISLKIANA 338

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Search completed: June 12, 2003, 08:49:12  
Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 12, 2003, 08:48:31 ; Search time 14 Seconds  
(without alignments)  
846,960 Million cell updates/sec

Title: US-09-412-100-23

Perfect score: 2079 1 MSMTSGICLASTMIGSIGA.....DAMAGDAINNALGKIGAA 403

Sequence: BL0SUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	100.0	403	2	US-08-200-724A-2
2	2079	100.0	403	2	US-09-030-270A-3
3	2079	100.0	403	4	US-08-851-376A-2
4	2079	100.0	403	4	US-08-984-207-3
5	2079	100.0	403	4	US-09-013-587-3
6	1928	92.7	385	1	US-08-891-254-3
7	1928	92.7	385	2	US-08-819-539-3
8	1928	92.7	385	5	PCT-US96-08819-3
9	1913	92.0	385	5	PCT-US93-06243-2
10	718.5	34.6	338	5	US-08-891-254-1
11	718.5	34.6	338	2	US-08-484-358-2
12	718.5	34.6	338	2	US-08-819-539-1
13	718.5	34.6	338	2	US-09-030-270A-1
14	718.5	34.6	338	3	US-08-118-959-2
15	718.5	34.6	338	4	US-08-984-207-1
16	718.5	34.6	338	4	US-09-013-587-1
17	718.5	34.6	338	4	PCT-US96-08819-1
18	211.5	10.2	651	4	US-09-060-756-727
19	211.5	10.2	651	4	US-08-556-978B-19
20	211.5	10.2	651	4	US-09-247-806-1
21	211.5	10.2	718	1	US-08-425-069-2
22	211.5	10.2	718	2	US-08-317-844B-2
23	211.5	10.2	747	3	US-09-034-177-3
24	206	9.9	604	4	US-08-556-978B-63
25	198.5	9.5	738	3	US-09-060-756-728
26	198.5	9.5	738	4	US-08-864-038A-3
27	198	9.5	606	4	US-09-247-806-6

28	197.5	9.5	344	1	US-08-891-254-7	Sequence 7, Appli
29	197.5	9.5	344	2	US-08-819-539-7	Sequence 7, Appli
30	197.5	9.5	344	2	US-09-030-270A-7	Sequence 7, Appli
31	197.5	9.5	344	4	US-08-984-207-7	Sequence 7, Appli
32	197.5	9.5	344	4	US-09-013-587-7	Sequence 7, Appli
33	197.5	9.5	344	4	PCT-US96-08819-7	Sequence 7, Appli
34	197	9.5	606	4	US-08-556-978B-23	Sequence 23, Appli
35	197	9.5	606	4	US-09-247-806-8	Sequence 8, Appli
36	194	9.3	1160	3	US-08-808-599A-24	Sequence 24, Appli
37	192.5	9.3	606	4	US-08-556-978B-21	Sequence 21, Appli
38	192.5	9.3	606	4	US-09-247-806-4	Sequence 4, Appli
39	190	9.1	641	1	US-09-249-585A-3	Sequence 3, Appli
40	186	8.9	749	1	US-08-317-522A-2	Sequence 2, Appli
41	186	8.9	749	1	US-08-439-818A-2	Sequence 2, Appli
42	186	8.9	749	2	US-08-751-965-2	Sequence 2, Appli
43	186	8.9	749	2	US-08-728-975-2	Sequence 2, Appli
44	186	8.9	749	2	US-08-728-626-2	Sequence 2, Appli
45	186	8.9	749	3	US-08-808-599A-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-200-724A-2  
; Sequence 2, Application US/08200724A  
; Patent No. 5849868  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Bauer, David W.  
; APPLICANT: Beer, Steven V.  
; APPLICANT: Collier, Alan  
; APPLICANT: He, Sheng-Yang  
; APPLICANT: Laby, Ron J.  
; TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE  
; NUMBER OF SEQUENCES: 5  
; TITLE OF INVENTION: IN PLANTS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentia Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/200,724A  
; FILING DATE: 23-FEB-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/10030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 403 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-200-724A-2  
; Query Match 100.0%; Score 2079; DB 2; Length 403;  
; Best Local Similarity 100.0%; Pred. No. 2.4e-174;  
; Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 403 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-851-376A-2

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 2.4e-174;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSLSLTSGIAGSTMOISIGAGGNNGLGTSRONAGLGNSALGLGGGNDTVNOLAGIL 60  
QY 61 TGMAMMSMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
DB 61 TGMAMMSMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TTSTNSPLDQALGINSTSQNDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGQDGT 180  
DB 121 TTSTNSPLDQALGINSTSQNDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGQDGT 180  
QY 181 QGSSSGGKOPTGEGONAKKGVTDALSGLMGNGLSQLLGNGLGGLGGGNGAGTGLDGSSL 240  
DB 181 QGSSSGGKOPTGEGONAKKGVTDALSGLMGNGLSQLLGNGLGGLGGGNGAGTGLDGSSL 240  
QY 241 GGGKGLONLSGPDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNGDRAMAKET 300  
DB 241 GGGKGLONLSGPDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNGDRAMAKET 300  
QY 301 GGFMDQYPEVFGKPOYQKGPQGVKTDKSNAKALSKPDDGMPASMEQFNKAKGMIR 360  
DB 301 GGFMDQYPEVFGKPOYQKGPQGVKTDKSNAKALSKPDDGMPASMEQFNKAKGMIR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNALGRLGAA 403  
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNALGRLGAA 403

RESULT 4  
US-08-984-207-3

; Sequence 3, Application US/08984207  
; Patent No. 6235974

GENERAL INFORMATION:

APPLICANT: Olu, Deven  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/984,207

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/033,230

FILING DATE: 05-DEC-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-984-207-3

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 2.4e-174;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSLTSGIAGSTMOISIGAGGNNGLGTSRONAGLGNSALGLGGGNDTVNOLAGIL 60  
DB 1 MSLSLTSGIAGSTMOISIGAGGNNGLGTSRONAGLGNSALGLGGGNDTVNOLAGIL 60  
QY 61 TGMAMMSMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
DB 61 TGMAMMSMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TTSTNSPLDQALGINSTSQNDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGQDGT 180  
DB 121 TTSTNSPLDQALGINSTSQNDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGQDGT 180  
QY 181 QGSSSGGKOPTGEGONAKKGVTDALSGLMGNGLSQLLGNGLGGLGGGNGAGTGLDGSSL 240  
DB 181 QGSSSGGKOPTGEGONAKKGVTDALSGLMGNGLSQLLGNGLGGLGGGNGAGTGLDGSSL 240  
QY 241 GGGKGLONLSGPDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNGDRAMAKET 300  
DB 241 GGGKGLONLSGPDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSSTRSFVNGDRAMAKET 300  
QY 301 GGFMDQYPEVFGKPOYQKGPQGVKTDKSNAKALSKPDDGMPASMEQFNKAKGMIR 360  
DB 301 GGFMDQYPEVFGKPOYQKGPQGVKTDKSNAKALSKPDDGMPASMEQFNKAKGMIR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNALGRLGAA 403  
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RESULT 5  
US-09-013-587-3

; Sequence 3, Application US/09013587  
; Patent No. 6277814

GENERAL INFORMATION:

APPLICANT: Olu, Deven  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/013,587

FILED DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,048  
FILING DATE: 27-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1501  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-013-587-3

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 2,4e-174;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLTSGIGASTMQLISIGAGGNNGLCTSRQNAIGLGSNLSALGCGNQNDTVNQLAGL 60  
DB 1 MSLTSGIGASTMQLISIGAGGNNGLCTSRQNAIGLGSNLSALGCGNQNDTVNQLAGL 60  
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DB 61 TGMAMMAMMGCGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TTSTNSPLDQALGINSTSONDSTSGTDSSTSDPMQOLLKMFSEIMQSLFGGQDGT 180  
DB 121 TTSTNSPLDQALGINSTSONDSTSGTDSSTSDPMQOLLKMFSEIMQSLFGGQDGT 180  
QY 181 QGSSGGKOPTREGONAKKGYTDALSGLMNGLSQLLGNGLGCGGCGNAGTGLDSSL 240  
DB 181 QGSSGGKOPTREGONAKKGYTDALSGLMNGLSQLLGNGLGCGGCGNAGTGLDSSL 240  
QY 241 GKGGLQNTSGPVDYQQLGNVGTGIGMAGIOALNDIGTHRSSSTRFVNGDRAMAEI 300  
DB 241 GKGGLQNTSGPVDYQQLGNVGTGIGMAGIOALNDIGTHRSSSTRFVNGDRAMAEI 300  
QY 301 GQFMQYFEVFGKPYQKPGQEVKTDKSNKALSKPDDGKMTFASMEQFNKAKGMIKR 360  
DB 301 GQFMQYFEVFGKPYQKPGQEVKTDKSNKALSKPDDGKMTFASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAIINNALLGKLGAA 403  
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAIINNALLGKLGAA 403

RESULT 6  
US-08-891-254-3  
Sequence 3, Application US/08891254  
Patent No. 5776889  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response  
TITLE OF INVENTION: Induced Resistance in Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,254  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-891-254-3

Query Match 92.7%; Score 1928; DB 1; Length 385;  
Best Local Similarity 100.0%; Pred. No. 3.8e-161;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLTSGIGASTMQLISIGAGGNNGLCTSRQNAIGLGSNLSALGCGNQNDTVNQLAGL 60  
DB 1 MSLTSGIGASTMQLISIGAGGNNGLCTSRQNAIGLGSNLSALGCGNQNDTVNQLAGL 60  
QY 61 TGMAMMAMMGCGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
DB 61 TGMAMMAMMGCGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TTSTNSPLDQALGINSTSONDSTSGTDSSTSDPMQOLLKMFSEIMQSLFGGQDGT 180  
DB 121 TTSTNSPLDQALGINSTSONDSTSGTDSSTSDPMQOLLKMFSEIMQSLFGGQDGT 180  
QY 181 QGSSGGKOPTREGONAKKGYTDALSGLMNGLSQLLGNGLGCGGCGNAGTGLDSSL 240  
DB 181 QGSSGGKOPTREGONAKKGYTDALSGLMNGLSQLLGNGLGCGGCGNAGTGLDSSL 240  
QY 241 GKGGLQNTSGPVDYQQLGNVGTGIGMAGIOALNDIGTHRSSSTRFVNGDRAMAEI 300  
DB 241 GKGGLQNTSGPVDYQQLGNVGTGIGMAGIOALNDIGTHRSSSTRFVNGDRAMAEI 300  
QY 301 GQFMQYFEVFGKPYQKPGQEVKTDKSNKALSKPDDGKMTFASMEQFNKAKGMIKR 360  
DB 301 GQFMQYFEVFGKPYQKPGQEVKTDKSNKALSKPDDGKMTFASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQ 372  
DB 361 PMAGDTGNGNLQ 372

RESULT 7  
US-08-819-539-3  
Sequence 3, Application US/08819539  
Patent No. 5859324  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response  
TITLE OF INVENTION: Induced Resistance in Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester

STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/819,539  
 FILING DATE: 17-MAR-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/475,775  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldman, Michael L.  
 REGISTRATION NUMBER: 30,727  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 263-1304  
 TELEFAX: (716) 263-1600  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 385 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-819-539-3

Query Match 92.7%; Score 1928; DB 2; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-161;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSINTSGLAGSTMOISIGAGAGNNGLGTSRONAGLGNSALGAGGNDNTVQIAGLL 60  
 1 MSINTSGLAGSTMOISIGAGAGNNGLGTSRONAGLGNSALGAGGNDNTVQIAGLL 60  
 61 TGMNMMMSMAGGGGIMGGGLGGLGNGIGSGGIGEGISNALNDMLAGSLTLTASKGGNN 120  
 61 TGMNMMMSMAGGGGIMGGGLGGLGNGIGSGGIGEGISNALNDMLAGSLTLTASKGGNN 120  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 241 GKGGLQNLISGPDVYQOLGNAVGTGIGKAGIOALNDIGTHRSSTRSFVNGDRAMAKEI 300  
 241 GKGGLQNLISGPDVYQOLGNAVGTGIGKAGIOALNDIGTHRSSTRSFVNGDRAMAKEI 300  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 361 PMAGDTGNGNIQ 372  
 361 PMAGDTGNGNIQ 372

RESULT 8  
 PCT-US96-08819-3

Sequence 3, Application PC/TUS9608819  
 GENERAL INFORMATION:  
 APPLICANT: Corneli Research Foundation, Inc.  
 TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
 TITLE OF INVENTION: RESISTANCE IN PLANTS  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 STREET: Clinton Square, P.O. Box 1051  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/08819  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/475,775  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldman, Michael L.  
 REGISTRATION NUMBER: 30,727  
 TELEPHONE: (716) 263-1304  
 TELEFAX: (716) 263-1600  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 385 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US96-08819-3

Query Match 92.7%; Score 1928; DB 5; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-161;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSINTSGLAGSTMOISIGAGAGNNGLGTSRONAGLGNSALGAGGNDNTVQIAGLL 60  
 1 MSINTSGLAGSTMOISIGAGAGNNGLGTSRONAGLGNSALGAGGNDNTVQIAGLL 60  
 61 TGMNMMMSMAGGGGIMGGGLGGLGNGIGSGGIGEGISNALNDMLAGSLTLTASKGGNN 120  
 61 TGMNMMMSMAGGGGIMGGGLGGLGNGIGSGGIGEGISNALNDMLAGSLTLTASKGGNN 120  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 121 TTTSTNSPLDQALGINSQNDSTSGTSTSDSDPMQQLKMFSEIMOSLFGDQDGT 180  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 181 OGSSSGKOPTEGEGONAKKGVTDALSGLMNGISQLLGNGLGGGGGAGNAGTGLDSSL 240  
 241 GKGGLQNLISGPDVYQOLGNAVGTGIGKAGIOALNDIGTHRSSTRSFVNGDRAMAKEI 300  
 241 GKGGLQNLISGPDVYQOLGNAVGTGIGKAGIOALNDIGTHRSSTRSFVNGDRAMAKEI 300  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 301 GGFMDQYEVFGKPYOKGPGQEVKTTDKSWAKALSKRPDDGMPASMEQFNKAKGMTR 360  
 361 PMAGDTGNGNIQ 372  
 361 PMAGDTGNGNIQ 372

RESULT 9  
 PCT-US93-06243-2

Sequence 2, Application PC/TUS9306243  
 GENERAL INFORMATION:  
 APPLICANT: Zhong-Min Wei, David W. Bauer, Steven V.  
 APPLICANT: Beer, Alan Collimer, Sheng-Yang He, and Ron J. Laby

;; TITLE OF INVENTION: Elicitor of the Hypersensitive Response in Plants  
;; NUMBER OF SEQUENCES: 5  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Yahwak & Associates  
;; STREET: 25 Skytop Drive  
;; CITY: Trumbull  
;; STATE: Connecticut  
;; COUNTRY: USA  
;; ZIP: 06611  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: Macintosh  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Microsoft Word 4.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/06243  
;; FILING DATE: 19930630  
;; CLASSIFICATION:  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: 907,935  
;; FILING DATE: 01-JUL-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: George M. Yahwak  
;; REGISTRATION NUMBER: 26,824  
;; REFERENCE/DOCKET NUMBER: CRF D-1172  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (203)268-1951  
;; TELEFAX: (203)268-1951  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 385 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; PCT-US93-06243-2

Query Match 92.0%; Score 1913; DB 5; Length 385;  
Best Local Similarity 99.5%; Pred. No. 7.9e-160;  
Matches 369; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSINTSGASTMQLSISGAGNNGLLGTSRONAGLGGNAGLGGGNDYVNOAGLL 60  
DB 1 MSINTSGASTMQLSISGAGNNGLLGTSRONAGLGGNAGLGGGNDYVNOAGLL 60  
QY 61 TGMAMMMAMGGGGLGGLGGGLGNGLGGSGGLGEGLSNALNDMLGSLINTLGSKGN 120  
DB 61 TGMAMMMAMGGGGLGGLGGGLGNGLGGSGGLGEGLSNALNDMLGSLINTLGSKGN 120  
QY 121 TSTTNSPLDQALGINSTSONDSTSGTSDTSDSSDPMOQLKMFSEIMOSLFGDGDGT 180  
DB 121 TSTTNSPLDQALGINSTSONDSTSGTSDTSDSSDPMOQLKMFSEIMOSLFGDGDGT 180  
QY 181 QCSSSSGKQPTREGQNAKYKGYTDALSGLMGNGLSOLLGNGLGGGCGGAGTGLDSSSL 240  
DB 181 QCSSSSGKQPTREGQNAKYKGYTDALSGLMGNGLSOLLGNGLGGGCGGAGTGLDSSSL 240  
QY 241 GKGGLGNTSGPYDQOLGNAVGTGIGMKAGIOLANDIGTHRSSTSFVKKGRAMAKEI 300  
DB 241 GKGGLGNTSGPYDQOLGNAVGTGIGMKAGIOLANDIGTHRSSTSFVKKGRAMAKEI 300  
QY 301 GGFMDQYPEVFGKPOYOKPGQEVKTDDSKMAKALSKPDDGKTPASMEQFNKAKGMIK 360  
DB 301 GGFMDQYPEVFGKPOYOKPGQEVKTDDSKMAKALSKPDDGKTPASMEQFNKAKGMIK 360  
QY 361 PMAGDTGNGNL 371  
DB 361 PMAGDTGNGNL 371

RESULT 10  
US-08-891-254-1  
; Sequence 1, Application us/08891254

;; Patent No. 5776889  
;; GENERAL INFORMATION:  
;; APPLICANT: Wei, Zhong-Min  
;; APPLICANT: Beer, Steven V.  
;; TITLE OF INVENTION: Hypersensitive Response  
;; TITLE OF INVENTION: Induced Resistance in Plants  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
;; STREET: Clinton Square, P.O. Box 1051  
;; CITY: Rochester  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 14603  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/891,254  
;; FILING DATE: 10-JUL-1997  
;; CLASSIFICATION: 514  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: 08/475,775  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldman, Michael L.  
;; REGISTRATION NUMBER: 30,727  
;; REFERENCE/DOCKET NUMBER: 14603/10050  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 263-1304  
;; TELEFAX: (716) 263-1600  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 338 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-891-254-1

Query Match 34.6%; Score 718.5; DB 1; Length 338;  
Best Local Similarity 42.8%; Pred. No. 2.8e-55;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOISI-GGAGNNGLLGTSRONAGLGG-NSA---LGLGNGNDYVNOAGLLTGMAMMM 67  
DB 1 MOITIAHIGGDLGVSGLGMO--GLGLNLSAASLSSVDKLSSTIDKTSALTSMV--- 55  
QY 68 SNAAGGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLINTLGSKGNNTTSTNS 127  
DB 56 -----FGGALAGSLGAS-SKGLGMSHQLGSGFN-----GAQASMLISVPK- 96  
QY 128 PLDQALGINSTSONDSTSGTSDTSDSSDPMOQLKMFSEIMOSLFG-----DQDQ 179  
DB 97 -----SGGDALS-----KMFALADLDLGHDTVTLTNSQ 128  
QY 180 TQSSSSGKQPTREGQNAKYKGYTDALSGLMGNGLSOLLGNGLGGGCGGAGTGLDSSSL 239  
DB 129 LANSMLNASQDTGNNAAFGSSGVNNAISLTLGGLGQSM-----SGFSQPS 174  
QY 240 LGGKGLONTSGPYDQOLGNAVGTGIGMKAGIOLANDIGTHRSSTSFVKKGRAMAKEI 299  
DB 175 LGAAGLQGLSGAFAFNDLGNALIMGYQONALNSLVSHTHYGNNRHFYDKEDRGAKKE 234  
QY 300 IGFMDQYPEVFGKPOYOKPGQEVKTDDSKMAKALSKPDDGKTPASMEQFNKAKGMIK 359  
DB 235 IGFMDQYPEIFFGKPEYOKKDGSSPKTDDSKMAKALSKPDDGKTPASMDKFRQAGMIK 294  
QY 360 RPAAGDTGNGNLQARGAGSSSLGTDAMMGDALNNNALGTLGA 403  
DB 295 SAVAGDTGNTNLNRGAGASLGTDAVAVGDKTANMSLGLANA 338





QY 300 IGFMDQPEYFGRKPOYOKPGSGEVKTDKSKAKALSRPDDGKTPASMEQFNKAKMIK 359  
DB 235 IGFMDQPEYFGRKPOYOKPGSGEVKTDKSKAKALSRPDDGKTPASMEQFNKAKMIK 294  
QY 360 RPAAGDTGNGNMQARGAGSSSLGIDAMAGDAINNMALGKICAA 403  
DB 295 SAVAGDTGNTNLNRGAGGASLGIDAAYVGDKIANNMSLGKLANA 338

RESULT 13  
US-09-030-270A-1

Sequence 1, Application US/09030270A

Patent No. 5977060

GENERAL INFORMATION:

APPLICANT: Zitter, Thomas A.

APPLICANT: Wei, Zhong-Min

TITLE OF INVENTION: INSECT CONTROL WITH A

TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans &amp; Doyle LLP

STREET: P.O. Box 1051, Clinton Square

CITY: Rochester

STATE: New York

COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,270A

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,226

FILING DATE: 28-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Michael L.

REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/1521

TELECOMMUNICATION INFORMATION:

TELEPHONE: (716) 263-1304

TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 338 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-030-270A-1

Query Match

Best Local Similarity 34.6%; Score 718.5; DB 2; Length 338;

Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOIST-GGAGGNNILGSTRONAGIG-NSA---LGAGGQNDTVNOLAGLNGMAMM 67  
DB 1 MOITIKAHIGDGLGVSGIAQ--GKGLNSAASSILGSSVDTLSITIDLTSLATSM--- 55  
QY 68 SMAGGGGLMGGGGLGAGGGLGSGGEGISNMLNDMLGSLNTLGSKGGNNNTTSTNS 127  
DB 56 -----FGGALAAQGLGAS-SKGLGMSNOLGQSGFGN---GAQGASNLLSVPK- 96  
QY 128 PLDQALGINSTQNDSTGTDSTSDSDPMQQLKMFSEIMQSLFG-----DQDQ 179  
DB 97 -----SGGDALS-----KMFDAKLDLGLHDVYTKLTNOSNQ 128  
QY 180 TGGSSSGKOPTGEEQNAKKGVYDALSGLMGNGLSQLLGNGGIGGCGGAGAGTGLDSS 239  
DB 180 TGGSSSGKOPTGEEQNAKKGVYDALSGLMGNGLSQLLGNGGIGGCGGAGAGTGLDSS 239

DB 129 LANSMLNSOMTQGMNAFSGCVNNALSSILGNGIGQSN-----SGFSQPS 174  
QY 240 LGCKGLQNLGSPVDYQOGLNNAVGTGIGMAGIOLNDICTHRSSSTRSPVNGDAMAKE 299  
DB 175 LGAGGLQGLSGAGANQGLNAGMKGVCQNALSLSNVSTHYDGNRRHFVDEKDGMAKE 234  
QY 300 IGFMDQPEYFGRKPOYOKPGSGEVKTDKSKAKALSRPDDGKTPASMEQFNKAKMIK 359  
DB 295 IGFMDQPEYFGRKPOYOKPGSGEVKTDKSKAKALSRPDDGKTPASMEQFNKAKMIK 294  
QY 360 RPAAGDTGNGNMQARGAGSSSLGIDAMAGDAINNMALGKICAA 403  
DB 295 SAVAGDTGNTNLNRGAGGASLGIDAAYVGDKIANNMSLGKLANA 338

RESULT 14  
US-09-118-959-2

Sequence 2, Application US/09118959

Patent No. 6001959

GENERAL INFORMATION:

APPLICANT: Bauer, David

APPLICANT: Collier, Alan

TITLE OF INVENTION: Hypersensitive Response Elicitor From

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans &amp; Doyle

STREET: Clinton Square

CITY: Rochester

STATE: New York

COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/118,959

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Michael L.

REGISTRATION NUMBER: 30,727

REFERENCE/DOCKET NUMBER: 19603/840

TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-263-1304

TELEFAX: 716-263-1600

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 338 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-118-959-2

Query Match

Best Local Similarity 34.6%; Score 718.5; DB 3; Length 338;

Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOIST-GGAGGNNILGSTRONAGIG-NSA---LGAGGQNDTVNOLAGLNGMAMM 67  
DB 1 MOITIKAHIGDGLGVSGIAQ--GKGLNSAASSILGSSVDTLSITIDLTSLATSM--- 55  
QY 68 SMAGGGGLMGGGGLGAGGGLGSGGEGISNMLNDMLGSLNTLGSKGGNNNTTSTNS 127  
DB 56 -----FGGALAAQGLGAS-SKGLGMSNOLGQSGFGN---GAQGASNLLSVPK- 96  
QY 128 PLDQALGINSTQNDSTGTDSTSDSDPMQQLKMFSEIMQSLFG-----DQDQ 179  
DB 97 -----SGGDALS-----KMFDAKLDLGLHDVYTKLTNOSNQ 128  
QY 180 TGGSSSGKOPTGEEQNAKKGVYDALSGLMGNGLSQLLGNGGIGGCGGAGAGTGLDSS 239  
DB 180 TGGSSSGKOPTGEEQNAKKGVYDALSGLMGNGLSQLLGNGGIGGCGGAGAGTGLDSS 239

Thu Jun 12. 14:55:49 2003

us-09-412-100-23.raii

Page 9

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QY 180 TQSSSSGKOPPEGGONNYYKKCVTALSLDMMNGSLQLLGNGLGGGGGGMNATGIDGSS 239
Db 129 LANSMLNASMOTQGMNNAFPGSGVNNALSSITLGNGLQSM-----SGSPQPS 174
QY 240 LGKGKGLQNLSGPVDYQOLGNNAVGTGIGMKACIOALNDICTGTHRRSSYRSPFNKGDRLMAKE 299
Db 175 LGAGGIGLGSGLGAENFOLGNALIGMGVGOAALSLNSVSTHYDGNRRHFPDKDRGMKE 234
QY 300 IGFQFDDQYFPEYFGKQYQKQPGQEQVKTDDKSNAKALSKFDDDGMTDPSMBQFNKATGMIT 359
Db 235 IGFQFDDQYFPEYFGKQYQKDGMSBSPRTDCKSNAKALSKFDDDGMTGASMDKFFQAGMGIK 294
QY 360 RPAAGDTGNGNLQARGAGSGSSLGIDPAMAAGDAPNNALFKLIGA 403
Db 295 SAVAGDTGNTNINLFGAGGASGLGIDPAAYVGDKLTANSLKRLANA 338

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RESULT 15  
 US-08-984-207-1  
 Sequence 1, Application US/08984207  
 Patent No. 6235974  
 GENERAL INFORMATION:  
 APPLICANT: Qiu, Deyuan  
 APPLICANT: Wei, Zhong-Min  
 APPLICANT: Beer, Steven V.  
 TITLE OF INVENTION: RESISTANT RESPONSE INDUCED  
 TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 STREET: P.O. Box 1051, Clinton Square  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/984,207  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/033,230  
 FILING DATE: 05-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldman, Michael L.  
 REGISTRATION NUMBER: 30,727  
 REFERENCE/DOCKET NUMBER: 19603/1201  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 263-1304  
 TELEFAX: (716) 263-1600  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 338 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-984-207-1

Query Match	34.6%	Score 718.5	DB 4	Length 338
Best Local Similarity	42.8%	Pred. No. 2.8e-55		
Matches 173; Conservative	41	Mismatches 111	Indels 79	Gaps 11

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OY      13 MOAISI -GAGAGGNNGLLGTSTRQNNAGLG -NSA---LGLGGGNONDTVNDLAGILLGMMMM 67
Db      1 MOTTIAHTIGGDVGSLGAQ--GLKGLNLSAASSLGSSVDKLSTVIDRLTSALTSMM--- 55
OY      68 SNAHGSGGIMCGGLGCGSLGNGLGGSGGLGRCNLNALNDMLGSLTNTLSKGKGNMTTSTNS 127
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Db 56 -----FGALAGIGAS -SKIGASNOIGASGN-----GAQASNILLSVPK - 96
QY 128 PLOALGINTSONDSTSTSTSTSHSSPMOOLIKHSEIMOSLFG-----DGDCG 178
Db 97 -----SGDALS-----KMDKALDILGHDYTKLTNOSNO 128
QY 180 TQSSSGCKPTEGEONAYKKCTVDLISGLANGSLISOLLGNGIGLGGGAGNAGTIDSS 233
Db 129 LANSMLNASOMTQGNNAAFEGSGVNNALSSILGGLGQSK-----SGFSQPS 178
QY 240 LGGGGLONTSGPVDYOOGLNAYVTGIGMARGIOLANDIGTRHSHSTBSFVYKGDRAAKE 299
Db 175 LGAGGIGLGLSGAGAFKOLGALISMGGONALISLANSVTHYDGNRRFVYKBERGAKE 234
QY 300 ICGPMDOYFEVEFSKPOYQKPGQEVYTDKSNAAKSKRPDDGKMPASMEQPNFNAKMIK 355
Db 235 ICGPMDOYFEIFKPEYOKDKWSSPPTDKDSNAKISKRDDDGKMGASMDKRFAMGMIK 299
QY 360 RPAAGDPTNGNLTQARGAGSSLGITDMMAGDGLNNALGRTIGAA 403
Db 295 SAVAGDTGNNTLMRGAGGASLGLIDAAYVGDGLTANSLGKLANA 338

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Search completed: June 12, 2003, 08:50:59  
Job time : 16 secs

Page 9



Db 181 QGSSSGGKQPTGEGBNAYKKGVTDALSGLMNGLSQLLGNGLGGGCGGAGNAGTGLDSSL 240  
QY 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
Db 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
QY 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360  
Db 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAJLCKLGA 403  
Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAJLCKLGA 403

## RESULT 2

US-09-086-118-23  
Sequence 23, Application US/09086118  
Patent No. US20010011380A1  
GENERAL INFORMATION:  
APPLICANT: Lady, Ronald J.  
APPLICANT: Beer, Steven V.  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
TITLE OF INVENTION: FRAGMENT ELICITING A HYPERSENSITIVE RESPONSE AND USES  
TITLE OF INVENTION: THEROP  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,118  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,109  
FILING DATE: 30-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1301  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-118-23

Query Match 100.0%; Score 2079; DB 10; Length 403;  
Best Local Similarity 100.0%; Pred. No. 9,5e-149;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLTSGIGASTMOISIGAGGNNGLGTSRONAGLGSNSALGIGGNNQNDTYNQLAGL 60  
Db 1 MSLLTSGIGASTMOISIGAGGNNGLGTSRONAGLGSNSALGIGGNNQNDTYNQLAGL 60  
QY 61 TGNMNMNMNGGGGGLMGGLGGGLGNGIGSSGGLGEGLSNALNDMLGGSINTLGSKGGNN 120  
Db 61 TGNMNMNMNGGGGGLMGGLGGGLGNGIGSSGGLGEGLSNALNDMLGGSINTLGSKGGNN 120

QY 121 TTSTNSPLDQALGINSTQNDSTSGTSDSSDPQQLKMFSEIMOSLFGDGQGT 180  
Db 121 TTSTNSPLDQALGINSTQNDSTSGTSDSSDPQQLKMFSEIMOSLFGDGQGT 180  
QY 181 QGSSSGGKQPTGEGBNAYKKGVTDALSGLMNGLSQLLGNGLGGGCGGAGNAGTGLDSSL 240  
Db 181 QGSSSGGKQPTGEGBNAYKKGVTDALSGLMNGLSQLLGNGLGGGCGGAGNAGTGLDSSL 240  
QY 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
Db 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
QY 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360  
Db 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAJLCKLGA 403  
Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAINNMAJLCKLGA 403

## RESULT 3

US-09-835-684-3  
Sequence 3, Application US/09835684  
Patent No. US20020019337A1  
GENERAL INFORMATION:  
APPLICANT: Qiu, Dewen  
APPLICANT: Remick, Dean  
TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE  
TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR  
FILE REFERENCE: 21829/71  
CURRENT APPLICATION NUMBER: US/09/835,684  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: 60/198,359  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 403  
TYPE: PRP  
ORGANISM: Erynia amylovora  
US-09-835-684-3

Query Match 100.0%; Score 2079; DB 10; Length 403;  
Best Local Similarity 100.0%; Pred. No. 9,5e-149;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLLTSGIGASTMOISIGAGGNNGLGTSRONAGLGSNSALGIGGNNQNDTYNQLAGL 60  
Db 1 MSLLTSGIGASTMOISIGAGGNNGLGTSRONAGLGSNSALGIGGNNQNDTYNQLAGL 60  
QY 61 TGNMNMNMNGGGGGLMGGLGGGLGNGIGSSGGLGEGLSNALNDMLGGSINTLGSKGGNN 120  
Db 61 TGNMNMNMNGGGGGLMGGLGGGLGNGIGSSGGLGEGLSNALNDMLGGSINTLGSKGGNN 120  
QY 121 TTSTNSPLDQALGINSTQNDSTSGTSDSSDPQQLKMFSEIMOSLFGDGQGT 180  
Db 121 TTSTNSPLDQALGINSTQNDSTSGTSDSSDPQQLKMFSEIMOSLFGDGQGT 180  
QY 181 QGSSSGGKQPTGEGBNAYKKGVTDALSGLMNGLSQLLGNGLGGGCGGAGNAGTGLDSSL 240  
Db 181 QGSSSGGKQPTGEGBNAYKKGVTDALSGLMNGLSQLLGNGLGGGCGGAGNAGTGLDSSL 240  
QY 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
Db 241 GKGGLQNLGSPVDYQQLGNNAVGTIGKAGIQAINDIGTHRSSTRFVNGDRAAKEI 300  
QY 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360  
Db 301 GGFMDQYPEVFGKPOYKQKPGQEVKTDKSWAKALSRPDDGMPASMEQFNKAKGMIKR 360

QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAIINNMAIGTGA 403  
|||||  
Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMAGDAIINNMAIGTGA 403

RESULT 4  
US-09-880-371-3

```

? Sequence 3 Application US/09880371
? Patent No. US20020059658A1
? GENERAL INFORMATION:
? APPLICANT: Wei, Zhong-Min
? APPLICANT: DeRoche, Jay
? TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
? TITLE OF INVENTION: PLANTS
? FILE REFERENCE: 21829/91
? CURRENT APPLICATION NUMBER: US/09/880,371
? CURRENT FILING DATE: 2001-06-13
? PRIOR APPLICATION NUMBER: 60/211,585
? PRIOR FILING DATE: 2000-06-15
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3
? LENGTH: 403
? TYPE: PRT
? ORGANISM: Erwinia amylovora
? US-09-880-371-3

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Query Match	100.0%	Score 2079;	DB 10;	length 403;
Best Local Similarity	100.0%;	Pred. No. 9, 5e-149;		
Matches 403; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	MSLNTSGAGATMQLISTGGAGGNNCLLSTRKNAIAGNSALGLGGGNQNDVYNOLAGLL	60
Db	1	MSLNTSGAGATMQLISTGGAGGNNCLLSTRKNAIAGNSALGLGGGNQNDVYNOLAGLL	60
QY	61	TGNAMAMSMGGGGLMGGGLGGGLANGLAGSSGGLGEGLSNALNDMLGSSLNTLTSKSGNN	120
Db	61	TGNAMAMSMGGGGLMGGGGLGGGLANGLAGSSGGLGEGLSNALNDMLGSSLNTLTSKSGNN	120
QY	121	TTSTTNSPLDALGINSTSQNDSTSGTSTSDSSDPMQOLLKMFSEIMQSLFGDQDGT	180
Db	121	TTSTTNSPLDALGINSTSQNDSTSGTSTSDSSDPMQOLLKMFSEIMQSLFGDQDGT	180
QY	181	QGSSSGGGQPIEGEGQNAKKKYVTYDALSGLMGNGLSQLLGNGLGGGGAGTGLDGSLL	240
Db	181	QGSSSGGGQPIEGEGQNAKKKYVTYDALSGLMGNGLSQLLGNGLGGGGAGTGLDGSLL	240
QY	241	GSGKGLQNTSGVDPYQQLGNNAVGTGIGMRAIGIALNDIGHRRSSSTRSFYNNKGRAMAKET	300
Db	241	GSGKGLQNTSGVDPYQQLGNNAVGTGIGMRAIGIALNDIGHRRSSSTRSFYNNKGRAMAKET	300
QY	301	GFPMDOYPEYFEGKPYQYKPGQEVYTDKSNAAKALSKPPDDGMPASMQDFNFAKMIKR	360
Db	301	GFPMDOYPEYFEGKPYQYKPGQEVYTDKSNAAKALSKPPDDGMPASMQDFNFAKMIKR	360
QY	361	PMAGDTGNGNTQARAGAGSSSLGIDPMAAGDAIANNALGTLGAA	403
Db	361	PMAGDTGNGNTQARAGAGSSSLGIDPMAAGDAIANNALGTLGAA	403

RESULT 5  
US-09-879-248-3  
Sequence 3, Application US/09879248  
Patent No. US20020062500A1  
GENERAL INFORMATION:  
APPLICANT: Fan, Hao  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 21829/81  
CURRENT APPLICATION NUMBER: US/09/879,248  
CURRENT FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/212,211  
 ;  
 ; PRIOR FILING DATE: 2000-06-16  
 ;  
 ; NUMBER OF SEQ ID NOS: 18  
 ;  
 ; SOFTWARE: PatentIn Ver. 2.1

ORGANISM: E  
US-09-879-248-3

Query Match	100.0%	Score 2079	DB 10	Length 403
Best Local Similarity	100.0%	Pred. No. 9.5e-149		
Matches 403	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	MSLNTSGAGATMGTGAGAGNNGLTSTSRQNGLGGSNSALGJGCGNQNTVNDLALGL	60	
Db	1	MSLNTSGAGATMGTGAGAGNNGLTSTSRQNGLGGSNSALGJGCGNQNTVNDLALGL	60	
OY	61	TGMNMMMSMGGGGLMGGLGGGLGNGLGSGGGLGEGLSNMLNDMLAGSLNTLTKSRGGNN	120	
Db	61	TGMNMMMSMGGGGLMGGLGGGLGNGLGSGGGLGEGLSNMLNDMLAGSLNTLTKSRGGNN	120	
OY	121	TTSTNTNSPLDALGINTSTSONDDSTSGTDSSTSDSSDPMOQLLKMFSEITMOSITFGDGQGT	180	
Db	121	TTSTNTNSPLDALGINTSTSONDDSTSGTDSSTSDSSDPMOQLLKMFSEITMOSITFGDGQGT	180	
OY	181	QGSSSGCKOPTEGEGONNAKKKVTVDALSGILMGNGLSQLGNGGLGGGCGNAGTGLDGSSL	240	
Db	181	QGSSSGCKOPTEGEGONNAKKKVTVDALSGILMGNGLSQLGNGGLGGGCGNAGTGLDGSSL	240	
OY	241	GKGGLQNTSGEVDYTOQLGNAVGTGKFAGIOALNDIGTTHRSSTRSEFVYNGDRAMAEI	300	
Db	241	GKGGLQNTSGEVDYTOQLGNAVGTGKFAGIOALNDIGTTHRSSTRSEFVYNGDRAMAEI	300	
OY	301	GOFMDQYEVYEGKIPQYOKGPOEYVTDKSNAAKLSKRPDDGMPASMEOPKAKGMIKR	360	
Db	301	GOFMDQYEVYEGKIPQYOKGPOEYVTDKSNAAKLSKRPDDGMPASMEOPKAKGMIKR	360	
OY	361	PMAGDTGNGNTQARGAGSSSLGIDAMMAGDAILNNALGRLGAA	403	
Db	361	PMAGDTGNGNTQARGAGSSSLGIDAMMAGDAILNNALGRLGAA	403	

RESULT 6  
US-09-770-693-3

Sequence 3 Application US/09770693  
Patent No. US20020069434A1  
GENERAL INFORMATION:  
APPLICANT: Beer, Steven V.  
APPLICANT: Bauer, David W.  
TITLE OF INVENTION: COMPOSITE-RESISTANT TRANSGENIC PLANTS BY VIRTUE OF  
TITLE OF INVENTION: PAHOEKEN-INDUCED EXPRESSION OF A HETEROLOGOUS  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
FILE REFERENCE: 19603/2501  
CURRENT APPLICATION NUMBER: US/09/770,693  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,565  
PRIOR FILING DATE: 2000-01-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 403  
TYPE: PRT  
ORGANISM: Erythrina amylovora  
US-09-770-693-3

Query Match	100.0%	Score 2079;	DB 10;	Length 403;
Best Local Similarity	100.0%	Pred. No. 9	5e-14;	
Matches 403: Conservative	0;	Mismatches	0;	Indels 0;

OY 1 MSLNTSGLGASTMQISIGGAGGNNGLCTSRQÑNAGLGNSALGIGGGNÖNDTVNQLAGLL 600  
|||||  
Db 1 MSLNTSGLGASTMQISIGGAGGNNGLCTSRQÑNAGLGNSALGIGGGNÖNDTVNQLAGLL 600

QY 61 TGMAMMAMGCGGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN 120  
DB 61 TGMAMMAMGCGGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN 120  
QY 121 TTSTNSPLDOLAGINSTSONDSTSGTDTSDSSDPMOQLLKMFSEIMOSLFGDGDGT 180  
DB 121 TTSTNSPLDOLAGINSTSONDSTSGTDTSDSSDPMOQLLKMFSEIMOSLFGDGDGT 180  
QY 181 OGSSSGGKOPTGEGONAYKKGYTDALSGLMGNGLSQLLGGNGLGGGOGGAGNAGTGLDSSSL 240  
DB 181 OGSSSGGKOPTGEGONAYKKGYTDALSGLMGNGLSQLLGGNGLGGGOGGAGNAGTGLDSSSL 240  
QY 241 GKGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 300  
DB 241 GKGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 300  
QY 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 360  
DB 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 360  
QY 361 PMAGDTGNGNLQANGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
DB 361 PMAGDTGNGNLQANGAGSSSLGIDAMAGDAINNMALGKLGAA 403

RESULT 7  
US-09-766-348-3  
; Sequence 3, Application US/09766348  
; Patent No. US20020116733A1  
; GENERAL INFORMATION:  
; APPLICANT: Qiu, Dwen  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Beer, Steven V.  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED RESISTANCE IN PLANTS BY  
; FILE REFERENCE: 19603/2986  
; CURRENT FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 08/984,207  
; PRIOR FILING DATE: 1997-12-03  
; PRIOR APPLICATION NUMBER: 60/033,230  
; PRIOR FILING DATE: 1996-12-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: *Ervinia amylovora*  
US-09-766-348-3

Query Match 100.0%; Score 2079; DB 10; Length 403;  
Best Local Similarity 100.0%; Pred. No. 9.5e-149;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MSNTSLGASTMISTIGGAGNGNLLGTSRONAGLGCNSALGIGGQNDNTVQLAGIL 60  
DB 1 MSNTSLGASTMISTIGGAGNGNLLGTSRONAGLGCNSALGIGGQNDNTVQLAGIL 60  
QY 61 TGMAMMAMGCGGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN 120  
DB 61 TGMAMMAMGCGGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN 120  
QY 121 TTSTNSPLDOLAGINSTSONDSTSGTDTSDSSDPMOQLLKMFSEIMOSLFGDGDGT 180  
DB 121 TTSTNSPLDOLAGINSTSONDSTSGTDTSDSSDPMOQLLKMFSEIMOSLFGDGDGT 180  
QY 181 OGSSSGGKOPTGEGONAYKKGYTDALSGLMGNGLSQLLGGNGLGGGOGGAGNAGTGLDSSSL 240  
DB 181 OGSSSGGKOPTGEGONAYKKGYTDALSGLMGNGLSQLLGGNGLGGGOGGAGNAGTGLDSSSL 240  
QY 241 GKGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 300  
DB 241 GKGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 300

DB 241 GKGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 300  
QY 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 360  
DB 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 360  
QY 361 PMAGDTGNGNLQANGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
DB 361 PMAGDTGNGNLQANGAGSSSLGIDAMAGDAINNMALGKLGAA 403

RESULT 8  
US-10-034-158-1  
; Sequence 1, Application US/10034158  
; Publication No. US20030028918A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: METHOD OF IMPARTING DROUGHT RESISTANCE TO PLANTS  
; FILE REFERENCE: 21829/230  
; CURRENT FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: 09/597,840  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: 09/013,587  
; PRIOR FILING DATE: 1998-01-26  
; PRIOR APPLICATION NUMBER: 60/036,048  
; PRIOR FILING DATE: 1997-01-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: *Ervinia chrysanthemi*  
US-10-034-158-1

Query Match 34.6%; Score 718.5; DB 9; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.4e-46;  
Matches 173; Conservative 41; Mismatches 11; Indels 79; Gaps 11;  
QY 13 MOISI-GGAGNNGLGTSNQMLGGS-NSA-...LGIGGQNDNTVQLAGILTGMMAMM 67  
DB 1 MOITIKAHIGDLGVSSIGLGAO-GLKGLNSAASSLGSVYKLSITDKLSALTSMM- 55  
QY 68 SMGCGGLMGGGLGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNNNTSTNS 127  
DB 56 -FGALAGLIGAS-SKGLGMSNGLGSGFN-...GAQASNLSTPK- 96  
QY 128 PLDOLAGINSTSONDSTSGTDTSDSSDPMOQLLKMFSEIMOSLFG-...DGQDG 179  
DB 97 -SGGDALS-...KMDKALDLDLGHDTYTKLTLNSQ 128  
QY 180 TCGSSSGKOPTGEGONAYKKGYTDALSGLMGNGLSQLLGGNGLGGGOGGAGNAGTGLDSS 239  
DB 129 LANSMLNASQPTQGNNAFSGVNNALSLTIGLGGSM-...SGFSDPS 174  
QY 240 LGKGLNLSGPDYQOOLGNVGTGIGMKAGIOLNDIGTHRSSTRSFVNGDRAMAKEY 299  
DB 175 LGAGGLGGLGAGFNLGNALIGKGYQONALSLSVTHYVGCNNHFTDKERGAKE 234  
QY 300 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 359  
DB 235 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSWAKLSRPDDGMPASMEQFNKAKMIKR 294  
QY 360 PMAGDTGNGNLQANGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
DB 295 SAVAGDTGNTNLNRGAGCASLIGIDAAVYGDRIANMISLGLANA 338

RESULT 9  
US-09-086-118-21  
; Sequence 21, Application US/09086118  
; Patent No. US20010011380A1  
; GENERAL INFORMATION:

```

APPLICANT: Lady, Ronald J.
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
TITLE OF INVENTION: FRAGMENT ELICITING A HYPERSENSITIVE RESPONSE AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hairgrave, Devans & Doyle LLP
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,118
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,109
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1301
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-118-21

Query Match      34.6%; Score 718.5; DB 10; Length 338;
Best Local Similarity 42.8%; Pred. No. 1.4e-46;
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOISI-GGAGGNNGLGTSRQNALGG-NSA---LGLGGGNDNTVQNLGLTGMMMM 67
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 1  MQITKAHIGGDLGVSGIAQ--GLKGLNSAASSLSSVSKLSTIDKLSALTSNM--- 55
QY 68 SMMGGGGLMGGGGLGGGGLGNGIGSGGGLGEGLSNLANLMDGLSLNTLSKSGGNNTTSTNS 127
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 56 -----FGALAGGLGAS-SKGLGMSNQLGSGFGN-----GAQASNLISVPK- 96
QY 128 PLDQALGINSTQNDSTSGTSDTSDDSPMQQLKFESEIMOSLFG-----DGODG 179
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 97 -----SGGDALS-----KMFDRALDDLGLHDVYTKLTLNSNQ 128
QY 180 TQSSSGGKOPTBEQONAYRKGYVDALSLGMLGNSQLLNGGLGCGGAGNAGTGLDSS 239
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 129 LANSMLNASQMTQGNNAFSGVNNALSLTGLNGLSM-----SGFSQPS 174
QY 240 LGGKGLNLSPVYDQOLGNAVGTGIGMKAGIOLNDIGTHRSSTRSFVNKGDRAMAKE 299
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 175 LGAGGLGSLGAGAFNOLGNAIGVGNALSLSVSTHVDGNHNFVDKEDRGMAKE 234
QY 300 IGFPMQDYPEVFGKPOYOKGPGQEVKTDDKSMARALSKPDDDCGTPASMEQFNKAGMIK 359
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 235 IGFPMQDYPEVFGKPEYOKGQWSSPKTDDKSWAALSKPDDDCGTPASMEQFNKAGMIK 294
QY 360 RPAAGDTGNGNLQARGAGSSSLGIDAMAGDAIINMALGKLGAA 403
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 295 SAVAGDTGNTNMLNRGAGASLIGDAVVDGKIANNMSIGKLGANA 338

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```

RESULT 10
US-09-835-684-1
Sequence 1, Application US/09835684
Patent No. US20020019337A1
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Qiu, Dewen
APPLICANT: Remick, Dean
TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
TITLE OF INVENTION: DESTICATION
FILE REFERENCE: 21829/71
CURRENT APPLICATION NUMBER: US/09/835,684
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/198,359
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 338
TYPE: PRT
ORGANISM: Erythra chrysanthemi
US-09-835-684-1

Query Match      34.6%; Score 718.5; DB 10; Length 338;
Best Local Similarity 42.8%; Pred. No. 1.4e-46;
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOISI-GGAGGNNGLGTSRQNALGG-NSA---LGLGGGNDNTVQNLGLTGMMMM 67
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 1  MQITKAHIGGDLGVSGIAQ--GLKGLNSAASSLSSVSKLSTIDKLSALTSNM--- 55
QY 68 SMMGGGGLMGGGGLGGGGLGNGIGSGGGLGEGLSNLANLMDGLSLNTLSKSGGNNTTSTNS 127
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 56 -----FGALAGGLGAS-SKGLGMSNQLGSGFGN-----GAQASNLISVPK- 96
QY 128 PLDQALGINSTQNDSTSGTSDTSDDSPMQQLKFESEIMOSLFG-----DGODG 179
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 97 -----SGGDALS-----KMFDRALDDLGLHDVYTKLTLNSNQ 128
QY 180 TQSSSGGKOPTBEQONAYRKGYVDALSLGMLGNSQLLNGGLGCGGAGNAGTGLDSS 239
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 129 LANSMLNASQMTQGNNAFSGVNNALSLTGLNGLSM-----SGFSQPS 174
QY 240 LGGKGLNLSPVYDQOLGNAVGTGIGMKAGIOLNDIGTHRSSTRSFVNKGDRAMAKE 299
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 175 LGAGGLGSLGAGAFNOLGNAIGVGNALSLSVSTHVDGNHNFVDKEDRGMAKE 234
QY 300 IGFPMQDYPEVFGKPOYOKGPGQEVKTDDKSMARALSKPDDDCGTPASMEQFNKAGMIK 359
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 235 IGFPMQDYPEVFGKPEYOKGQWSSPKTDDKSWAALSKPDDDCGTPASMEQFNKAGMIK 294
QY 360 RPAAGDTGNGNLQARGAGSSSLGIDAMAGDAIINMALGKLGAA 403
    |||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|  ||:|
Db 295 SAVAGDTGNTNMLNRGAGASLIGDAVVDGKIANNMSIGKLGANA 338

RESULT 11
US-09-880-371-1
Sequence 1, Application US/09880371
Patent No. US20020059658A1
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: DeRoche, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 21829/91
CURRENT APPLICATION NUMBER: US/09/880,371
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,585
PRIOR FILING DATE: 2000-06-15

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NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Erwinia chrysanthemi  
US-09-880-371-1

Query Match 34.6%; Score 718.5; DB 10; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.4e-46;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

QY 13 MOISI-GGAGGNNGLTSTRONAGLIG-NSA---LGLGGGNDNTVNOAGLLTGMMMM 67  
DB 1 MOTIRKAHIGDGLVSGLAGO--GLKGLNSAASSLGSSVDKLSSTIDKLTSTALTSMM-- 55  
QY 68 SMAGGGGLMGGGLGGGNGIGSGGGLGEGLSNLTNDMLGSLTWTLSKGGKGNNTTSTNS 127  
DB 56 -----FGALAAQGLIGAS-SKGLGMSNOLGSGFGN-----GAGASNLISVPRK- 96  
QY 128 PLDQALGINTSQNDSTSGTSDTSDDSPMOQLLKPFSEIMOSLFG-----DQDQG 179  
DB 97 -----SGGDALS-----KMFDRKALDLDLGHDTYTKLTNSQ 128  
QY 180 TCGSSSGKOPTGEONAYKKGYTDALSGLMGNGLSQLLNGGIGGGGAGAGTGLDSS 239  
DB 129 LANSMLNASQMTQGNMNAFGSGVNNALSLILNGLSGSM-----SGFSQPS 174  
QY 240 LGAGGLONLSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSTRSFYVNGGRAMAKE 299  
DB 175 LGAGGLGGLSGAGAFNGLGNLIGMGVGNALSLSVSTHYDGNNNHFFVDKEDRGMAKE 234  
QY 300 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 359  
DB 235 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 294  
QY 360 RPMAGDTGNGMLQARGAGSSSLGIDAMAGDAINNMLGKIGAA 403  
DB 295 SAVAGDTGNTNLNRGAGGASLIGIDAAYVGDKIANNMISLGIKLANA 338

RESULT 12  
US-09-879-248-1  
Sequence 1, Application US/09879248  
Patent No. US20020062500A1  
GENERAL INFORMATION:  
APPLICANT: Fan, Hao  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 21829/81  
CURRENT APPLICATION NUMBER: US/09/879, 248  
CURRENT FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/212,211  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Erwinia chrysanthemi  
US-09-879-248-1

Query Match 34.6%; Score 718.5; DB 10; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.4e-46;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;  
QY 13 MOISI-GGAGGNNGLTSTRONAGLIG-NSA---LGLGGGNDNTVNOAGLLTGMMMM 67  
DB 1 MOTIRKAHIGDGLVSGLAGO--GLKGLNSAASSLGSSVDKLSSTIDKLTSTALTSMM-- 55  
QY 68 SMAGGGGLMGGGLGGGNGIGSGGGLGEGLSNLTNDMLGSLTWTLSKGGKGNNTTSTNS 127

DB 56 -----FGALAAQGLIGAS-SKGLGMSNOLGSGFGN-----GAGASNLISVPRK- 96  
QY 128 PLDQALGINTSQNDSTSGTSDTSDDSPMOQLLKPFSEIMOSLFG-----DQDQG 179  
DB 97 -----SGGDALS-----KMFDRKALDLDLGHDTYTKLTNSQ 128  
QY 180 TCGSSSGKOPTGEONAYKKGYTDALSGLMGNGLSQLLNGGIGGGGAGAGTGLDSS 239  
DB 129 LANSMLNASQMTQGNMNAFGSGVNNALSLILNGLSGSM-----SGFSQPS 174  
QY 240 LGAGGLONLSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSTRSFYVNGGRAMAKE 299  
DB 175 LGAGGLGGLSGAGAFNGLGNLIGMGVGNALSLSVSTHYDGNNNHFFVDKEDRGMAKE 234  
QY 300 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 359  
DB 235 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 294  
QY 360 RPMAGDTGNGMLQARGAGSSSLGIDAMAGDAINNMLGKIGAA 403  
DB 295 SAVAGDTGNTNLNRGAGGASLIGIDAAYVGDKIANNMISLGIKLANA 338

RESULT 13  
US-09-770-693-1  
Sequence 1, Application US/09770693  
Patent No. US20020069434A1  
GENERAL INFORMATION:  
APPLICANT: Baer, Steven V.  
APPLICANT: Bauer, David W.  
TITLE OF INVENTION: COMETE-RESISTANT TRANSGENIC PLANTS BY VIRTUE OF  
TITLE OF INVENTION: PATOGEN-INDUCED EXPRESSION OF A HETEROLOGOUS  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
FILE REFERENCE: 19603/2501  
CURRENT APPLICATION NUMBER: US/09/770, 693  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,565  
PRIOR FILING DATE: 2000-01-26  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Erwinia chrysanthemi  
US-09-770-693-1

Query Match 34.6%; Score 718.5; DB 10; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.4e-46;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;  
QY 13 MOISI-GGAGGNNGLTSTRONAGLIG-NSA---LGLGGGNDNTVNOAGLLTGMMMM 67  
DB 1 MOTIRKAHIGDGLVSGLAGO--GLKGLNSAASSLGSSVDKLSSTIDKLTSTALTSMM-- 55  
QY 68 SMAGGGGLMGGGLGGGNGIGSGGGLGEGLSNLTNDMLGSLTWTLSKGGKGNNTTSTNS 127  
DB 56 -----FGALAAQGLIGAS-SKGLGMSNOLGSGFGN-----GAGASNLISVPRK- 96  
QY 128 PLDQALGINTSQNDSTSGTSDTSDDSPMOQLLKPFSEIMOSLFG-----DQDQG 179  
DB 97 -----SGGDALS-----KMFDRKALDLDLGHDTYTKLTNSQ 128  
QY 180 TCGSSSGKOPTGEONAYKKGYTDALSGLMGNGLSQLLNGGIGGGGAGAGTGLDSS 239  
DB 129 LANSMLNASQMTQGNMNAFGSGVNNALSLILNGLSGSM-----SGFSQPS 174  
QY 240 LGAGGLONLSPVDYQOLGNAVGTGIGMKAGIQALNDIGTHRSSTRSFYVNGGRAMAKE 299  
DB 175 LGAGGLGGLSGAGAFNGLGNLIGMGVGNALSLSVSTHYDGNNNHFFVDKEDRGMAKE 234  
QY 300 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 359  
DB 235 IGFMDQYPEYFGAPYOKGPGQEVKTDDKSMARALSKPDDGKTPASMDQFNKAKMIK 294

Page 7

RESULT 15  
US-09-820-843A-20  
; Sequence 20. Application US/09820843A  
; Publication No. US20030039963A1  
; GENERAL INFORMATION:  
; APPLICANT: Council of Scientific and Industrial Research  
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEINS  
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES  
; FILE REFERENCE: 063915

Search completed: June 12, 2003, 08:51:27  
Job time : 24 secs











A:Cross-references: GB:280225; GB:AL123456; MID:g3261265; PIDN:CAB02341.1; PID:e266390;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV2634c  
C:Superfamily: unassigned collagens

Query Match 11.6%; Score 242; DB 2; Length 778;  
Best Local Similarity 30.18; Pred. No. 6.9e-08;  
Matches 91; Conservative 19; Mismatches 110; Indels 82; Gaps 14;

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QY 7 GLGASTWQISIGAG--GNNGLGTSRONAGLGSNSALGIG--GNNDYVQNLGL 60
DB 353 GNGNNMWFSSGAGGCGCTGAGTNGVNSIANTPTGANGDNGSGNOT----- 404
QY 61 TGMAMMMWMMGGGGLMGGLG--NGIGSGGLGEGLSNLMNMLGSLNTLWGSKG 118
DB 405 -----GNG--GPGPAGGVGAGVGCGGGLGESLDG--NQTGG-----KGG 443
QY 119 NNTSTTNSPLDQALGINTSNDSTSGTSTSDSSDPQOLKMFSEIMOSLEFGDGD 178
DB 444 AGGTAGTGDGAGAGAGGIGETDGSAGV-----ATGCGGCD 481
QY 179 GTGSSSGCKPTEGE-QNAFKKVTDAL--SLMGNG--LSQLLNGSLG----- 225
DB 482 GATGCVDGVGAGAGKCGCHMTGVDATFGDGLGEGALGAMGNGGTGAGGNGG 541
QY 226 -----GCGNACTGLDSSLGKGLONLSGPV---DYQOLGNVGTGIGKAGIQLMND 276
DB 542 RGMGLGNGGAGGAGGTGT--GGGGAAGFAGVGAGGGBELTGTGAGTAGEGTGLGSLG 600
QY 277 IG 278
DB 601 VG 602
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## RESULT 13

hypothetical glycine-rich protein RV0278c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence.revision 17-Jul-1998 #text.change 20-Jun-2000  
C:Accession: D70835  
R:Coile, S.T.; Brosch, R.; Parish, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MID:98295987; PMID:9634230  
A:Accession: D70835  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-957 <COL>  
A:Cross-references: GB:AL021930; GB:AL123456; MID:g3261524; PIDN:CA17353.1; PID:g290946  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV0278c  
C:Superfamily: elastin

Query Match 11.6%; Score 241.5; DB 2; Length 957;  
Best Local Similarity 25.8%; Pred. No. 9.4e-08;  
Matches 117; Conservative 42; Mismatches 149; Indels 145; Gaps 21;

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QY 2 SLTSTGLASTWQISIGAGGNGGLGTSRONAGLGG--NSALGIGGNGNDYVQNL 57
DB 362 TLVAGTIGCA-----GAGAGNAGLIFGSGSGAGGFPADGCGGPGCN-----A 407
QY 58 GILTGMMMMWMMGGGGLMG--GGLGGLGSLNGLGSSGL-----GGLSNAL--N 103
DB 408 G-----TVFGSGAGGNGGVGCGFAGIGAGCTPCLLNGNGGNGGASAVYGCN 458
QY 104 DMLGSLNTLWGSKGNNSTTNSPLDQALGINTSNDSTSGTSTSDSSDPQOLK 163
DB 459 GGIGGTGVLIGN--GNGGSGGIGAKAGVGSGLLGLDGFNAPASTSLHTLQDNVLA 517
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QY 164 MFSEIMOS-----LFGDGODGTGGS-----SSGKQPTGEBQNAFKKVTDALSG-LMGNG 213
DB 518 VVNEPPTLGRPLRIGNANTPRTGADGAGGGLFNGANGTGTCTGAGAGGWLTMNG 577
QY 214 LSQLLNGGLG-----GCGNAGTGLDSSLGKGLONLSGPVY 254
DB 578 -----GNGCHGATNTAATATGAGAGGILFEGTGNGGTG--GIATGAGGIGAGAGGV 630
QY 255 QQLGNAYGTG-----IGMKAGIOLMNDIGHHSSTRSRVYKCDRMAKEIGOPMDQYP 308
DB 631 SLTIGSGGTGNGNSIGV--AGIGAGGCG-----GDACL----- 664
QY 309 EVEGKPOYKPGCEVETDCKSMALKSKPDDDCMTAPSMEOQFKAKGMIKRPAGPTGN 368
DB 665 LFG-----ACTGC-----HGAAGVPAGVGAGGN 690
QY 369 GNLOAKAGAGSSSLGIDMAMGDAINNALKL 401
DB 691 GGLFANGAGAGGAFNA--AGNGNGGLFETGG 722
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## RESULT 14

hypothetical glycine-rich protein RV1840c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence.revision 17-Jul-1998 #text.change 20-Jun-2000  
C:Accession: H70663  
R:Coile, S.T.; Brosch, R.; Parish, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MID:98295987; PMID:9634230  
A:Accession: H70663  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-515 <COL>  
A:Cross-references: GB:283859; GB:AL123456; MID:g3261678; PIDN:CAB06114.1; PID:g1781  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV1840c  
C:Superfamily: Phaseolus glycine-rich cell wall protein 1.8

Query Match 11.5%; Score 238.5; DB 2; Length 515;  
Best Local Similarity 27.38; Pred. No. 7.1e-08;  
Matches 109; Conservative 23; Mismatches 128; Indels 139; Gaps 15;

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QY 18 GAGGNGGLGTSRONAGLGSNSALGIGGNGNDYVQNLGLTGMMMMWMMGGGGLMG 77
DB 148 GAGGAGDAGLIGN--GNGIGGPGPATGLAG-----AGVGGLLFGDGGNGAGGLG 197
QY 78 GGLGGLGSLNGLGSGLGEGLSNLMNMLGSLNTLWGSKGNNSTTNSPL--DQNLGI 135
DB 198 TGPVGATG--GIGGPGCAAVGLFCHGAGAGGLAKAGFAGAGGTGTGLLNGNGNG 256
QY 136 NSTSONDSTSGTSTSDSSDPQOLKMFSEIMOSLFGGCGGTGCGSSSGGKQPTGEGQ 195
DB 257 NVBSGADGAGGGA-----RLTNGCGG-----GSVGAAPG-- 289
QY 196 NAYKGVTDALSLGMLNGSLQLGNGGLG--GCGNACTGLDSSLGKGLONLSGPV 252
DB 290 -----IGNG-----GNGNGCMLTGDDSGSGSTLGTGSDGTG----- 322
QY 253 DYQOLGNVGTGIGMAGIOLMNDIGHHSSTRSRVYKCDRMAKEIGOPMDQYEVFG 312
DB 323 -----GNAAGFPGGNGGFEFFDNGGDDGTGLLIGNGD----- 358
QY 313 KPOYKPGGPEVETDCKSMALKSKPDDDCMTAPSMEOQFKAKGMIKRPAGPTGN-- 368
DB 359 -----GNSVPTD-----GFL--RGHGCGGAGNAVGL 382
```





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 12, 2003, 08:46:41 ; Search time 11 Seconds

(Without alignments)  
1519.542 Million cell updates/sec

Title: US-09-412-100-23

Perfect score: 2079  
Sequence: 1 MSINTSGIGASTMOISIGGA.....DAMWAGDAINNMALGKLGAA 403

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	2050	98.6	403	1	HRPN_ERWAM
2	838.5	39.9	356	1	HRPN_ERMCA
3	718.5	34.6	340	1	HRPN_ERMCH
4	248	11.9	463	1	YAB8_MYCRU
5	242	11.6	778	1	YQ34_MYCRU
6	241.5	11.6	957	1	Y278_MYCRU
7	238.5	11.5	515	1	Y140_MYCRU
8	238	11.4	1901	1	Y208_MYCRU
9	235.5	11.3	914	1	WA22_MYCRU
10	234.5	11.3	543	1	YP91_MYCRU
11	233.5	11.2	338	1	GRP_ARATH
12	232	11.2	801	1	Y747_MYCRU
13	229.5	11.0	603	1	YD25_MYCRU
14	229	11.0	491	1	YR98_MYCRU
15	214.5	10.3	384	1	GRP1_PERYT
16	213.5	10.3	481	1	LORI_MOUSE
17	211.5	10.2	747	1	SPD1_MOUSE
18	210	10.1	1156	1	GLH4_CAEEL
19	202.5	9.7	97	1	Y118_MYCRU
20	199	9.6	937	1	HRP1_CANAL
21	187.5	9.5	344	1	POPA_RALSO
22	196.5	9.5	465	1	GRP2_PHAVU
23	193	9.3	183	1	GRP2_ORYSA
24	191	9.2	252	1	GRP1_PHAVU
25	191	9.2	316	1	LORI_HUMAN
26	190	9.1	641	1	ERN1_EBV
27	186.5	9.0	1113	1	N116_YEAST
28	186	8.9	1387	1	TRDP_HUMAN
29	184.5	8.9	419	1	CSP_PLACB
30	178.5	8.6	959	1	N100_YEAST
31	177.5	8.5	1224	1	PER_DROME
32	175.5	8.4	734	1	YR2_CAEEL
33	174.5	8.4	672	1	PHX5_MOUSE

34	174	8.4	212	1	EGG1_SCHUA	P19470 schistosoma
35	174	8.4	700	1	NOMA_DROME	O04047 drosophila
36	173.5	8.3	1380	1	DDX9_MOUSE	O70133 mus musculus
37	172	8.3	5263	1	FROH_BOMO	P05790 bombyx mori
38	171.5	8.2	1208	1	PER_DROVA	Q24767 drosophila
39	169	8.1	526	1	FUS_HUMAN	P35637 homo sapien
40	169	8.1	1596	1	NAM_DROME	P21519 drosophila
41	167	8.0	401	1	CSP_PLACB	P08674 plasmodium
42	166.5	8.0	393	1	CSP_PLACB	P14593 plasmodium
43	165.5	8.0	207	1	EGG2_SCHUA	P19469 schistosoma
44	164.5	7.9	404	1	CAZ_DROME	Q27294 drosophila
45	164	7.9	518	1	FUS_MOUSE	P56959 mus musculus

## ALIGNMENTS

RESULT 1	HRPN_ERWAM	STANDARD:	PRT:	403 AA.
ID	HRPN_ERWAM			
AC	001099:			
DT	01-APR-1993 (Rel. 25, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Harpin (Harpin-EA).			
GN	HRPN.			
OS	Erwinia amylovora.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OX	Erwinia.			
NCBI_TaxID=552;				
RM	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.			
RC	STRAIN-Ea321:			
RX	MEDLINE-92320301; PubMed-1621099;			
RA	Wei Z.-M., Lady R.J., Zumoff C.H., Bauer D.W., He S.Y., Collmer A.,			
RA	Beer S.V.;			
RT	"Harpin, elicitor of the hypersensitive response produced by the			
RT	plant pathogen Erwinia amylovora.";			
RL	Science 257:85-88(1992).			
RN	[2]			
RP	REVIEWS.			
RC	STRAIN-Ea321:			
RA	Lady R.J., Kim J.F., Beer S.V.;			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT			
CC	UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO			
CC	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.			
CC	-1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
DR	EMBL; M92994; AAC31644.2; -			
KW	Hypersensitive response.			
FT	DOMAIN 1 270			
FT	DOMAIN 63 70			
FT	SEQUENCE 403 AA; 39697 MW; 146FA642351DBE87 CRC64;			
QY	Query Match	98.6%;	Score 2050;	DB 1; Length 403;
QY	Best Local Similarity	99.0%;	Pred. No. 3e-115;	
QY	Matches 399;	Conservative	0;	Mismatches 4;
QY			Indels	0;
QY			Gaps	0;
DB	1 MSINTSGIGASTMOISIGGAGNGGLGTSRONAGLGNSALGLGGGNDPTVNOIAGIL	60		
DB	1 MSINTSGIGASTMOISIGGAGNGGLGTSRONAGLGNSALGLGGGNDPTVNOIAGIL	60		
QY	61 TGMNDMMSMGGGGLMGGLGGGLGGLGSGGLGEGLSNLDMDAGSLMTLGSKGGNN	120		

Db 61 TGMHMMHMMGGGGLMGGLGGLGNGLGSGGLGEBLSNANLMDLGSINTLGSKGN 120  
 Qy 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPMOQLKMFSEIMOSLFEDGDGT 180  
 Db 121 TTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPMOQLKMFSEIMOSLFEDGDGT 180  
 Qy 181 OGSSSGKOPTEGEONAYKKGVDALSGLMNGLSQLLNGNGLGCGGCGNAGTGLDSSL 240  
 Db 181 OGSSSGKOPTEGEONAYKKGVDALSGLMNGLSQLLNGNGLGCGGCGNAGTGLDSSL 240  
 Qy 241 GKGGLQNLGSPVDYQQLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFVYKNGDRAMKEI 300  
 Db 241 GKGGLQNLGSPVDYQQLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFVYKNGDRAMKEI 300  
 Qy 301 GOFMDQPEYFVGKPOYKPGQEVKTDKSNAAKLSPPDDGKTPASMEQFNKAKIKR 360  
 Db 301 GOFMDQPEYFVGKPOYKPGQEVKTDKSNAAKLSPPDDGKTPASMEQFNKAKIKR 360  
 Qy 361 PMAGDTGNGMLQARGAGSSSLGIDAMAGDAINNMALGKLGAA 403  
 Db 361 AMAGDTGNGMLQARGAGSSSLGIDAMAGDAINNMALGKLGAA 403

## RESULT 2

HRPN\_ERMCA

ID HRPN\_ERMCA STANDARD: PRT: 356 AA.

AC 047278;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Harpin (Harpin-ECC) (Fragment).  
 GN HRPN.  
 OS Erwinia carotovora.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Pectobacterium.  
 OX NCBI\_TaxID=554;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=71;  
 RX MEDLINE=96405946; PubMed=8810071;  
 RA Cai Y., Madl L., Mukherjee A., Dumenyo C.K., Chatterjee A.K.;  
 RT "The RsmA-mutants of Erwinia carotovora subsp. carotovora strain  
 RT Ec971 overexpress hrpNcc and elicit a hypersensitive reaction-like  
 RT response in tobacco leaves.";  
 RL Mol. Plant Microbe Interact. 9:565-573(1996).  
 CC -1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT  
 CC UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO  
 CC REQUIRED FOR PATHOGENICITY IN HOST PLANTS.  
 CC -1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.  
 CC  
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 CC  
 DR EMBL: L78834; ABA49733.1;  
 KM Hypersensitive response.  
 FT DOMAIN 1 224 GLY-RICH.  
 FT NON\_TER 356 356  
 SQ SEQUENCE 356 AA; 108BA6B9D27F9DE4 CRC64;

Query Match 39.9%; Score 828.5; DB 1; Length 356;  
 Best Local Similarity 48.2%; Pred. No. 9.4e-43;  
 Matches 196; Conservative 37; Mismatches 115; Indels 59; Gaps 11;

Qy 3 LNTSGAGASTMOISIGAGGNNGLT-GTSHQNGLGNSALGLGCGNNDVTYNQALGLT 61  
 Db 2 LNSIGGAS-LQITTI-KAGNGGLFPPSSONSNGSPSOSAF---GGRSNIARQLSDIMT 56  
 Qy 62 GMMHMMHMMGGGGLMGGLGGLGNGLGSGGLGEBLSNANLMDLGSINTLGS 115

Db 57 TMMFMGSMWGG--MSGGLGGLGSSLGGLGGLG-GGLGGLGSSLGSGLSALG--CG 111  
 Qy 116 KGNNTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPMOQLKMFSEIMOSLFED 175  
 Db 112 LGC-----ALGAMNMANPSSAMNGS-----LFSALEDLG 143  
 Qy 176 GDDTQSSSGKOPTEGEONAYKKGVDALSGLMNGLSQLLNGNGLGCGGCGNAGTGL 235  
 Db 144 GMSQGGGLGNGKPPSSPEISATYQGVNDALSLGNGLSQTKQ-----T 189  
 Qy 236 DGSGLGKGLQNLGSPVDYQQLGNAVGTGIGMKAGIOLANDIGTHRSSTRSFVYKNGDR 295  
 Db 190 SPQLGNNGLQGLSGAGAFNQLGSLGMSVQKAGLELNNISITHNDSPRYFYDKEDRG 249  
 Qy 296 MAKEIGFMOYPEYFVGKPOYKPGQEVKTDKSNAAKLSPPDDGKTPASMEQFNKAK 355  
 Db 250 MAKEIGFMOYPEYFVGKPOYKPGQEVKTDKSNAAKLSPPDDGKTPASMEQFNKAK 309  
 Qy 356 GMKRPAGDTGNGMLQARGAGSSSLGIDAMAGDAINNMALGKLGAA 402  
 Db 310 GMKRSATRGDTGNGMLQARGAGSSSLGIDAMAGDAINNMALGKLGAA 356

## RESULT 3

HRPN\_ERMCH

ID HRPN\_ERMCH STANDARD: PRT: 340 AA.

AC 047278;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Harpin (Harpin-ECH).  
 GN HRPN.  
 OS Erwinia chrysanthemi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Pectobacterium.  
 OX NCBI\_TaxID=556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EC16 / AC1450;  
 RX MEDLINE=96172740; PubMed=8589405;  
 RA Bauer D.W., Wei Z.M., Beer S.V., Collmer A.;  
 RT "Erwinia chrysanthemi harpinch: an elicitor of the hypersensitive  
 RT response that contributes to soft-rot pathogenesis.";  
 RL Mol. Plant Microbe Interact. 8:484-491(1995).  
 CC -1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT  
 CC UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO  
 CC REQUIRED FOR PATHOGENICITY IN HOST PLANTS.  
 CC -1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.  
 CC  
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 CC  
 DR EMBL: L39897; AAC31978.1;  
 KM Hypersensitive response.  
 FT DOMAIN 1 203 GLY-RICH.  
 FT NON\_TER 340 340  
 SQ SEQUENCE 340 AA; 34274 MW; E4D82C23731EF4C5 CRC64;

Query Match 34.6%; Score 718.5; DB 1; Length 340;  
 Best Local Similarity 42.6%; Pred. No. 3.1e-36;  
 Matches 172; Conservative 41; Mismatches 114; Indels 77; Gaps 10;

Qy 13 MOIST-GGAGGNNGLTSTSHQNGLG-NSA---LGLGCGNNDVTYNQALGLTGMAMM 67  
 Db 1 MQITKHHIGDGLVSGIGLAGGLKLNBAASSVSKSTIDKLSALTSM--- 57  
 Qy 68 SMHGGGGLMGGLGGLGNGLGSGGLGEBLSNANLMDLGSINTLGSKGNNTSTNS 127

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Db      58 -----FCGALAGLGAS-SKGLGMSNOLGOSFGN-----GAQAGSNLLSVRK- 98
OY      128 PLDQALGINSTGNDSTGTDSTSDSDPMQQLKMFSEIMQSLFG-----DGDG 179
Db      99 -----SGDALS-----KMFEDKALDDLIGDPTVTKLINSQ 130
OY      180 TCGSSSGKOPTEGEQNAKKGYVDALSGLMGNGLSQLLNGNGLGCGGCGNAGTGLDSS 239
Db      131 LANSMLNLSQMTQGMNAFGSGVNNALSLILNGLSQSN-----SGFSOPS 176
OY      240 LGKGLQNLGSPVYDQQLGNNVGTGIGKAGIOLALNDLGTNRHSRSPYNNKDRAMAKE 299
Db      177 LGAGLGGLSGAGAFNQGLMAGMGVGNALSLALSNVSTHYDGNRRHVEDKEDGMAKE 236
OY      300 IGFPMDOYPEYFGRKQYQKPGQEVKTDKSNKALSKPDDGDMTPASMEQENKAKMIX 359
Db      237 IGFPMDOYPEYFGRKQYQKPGQEVKTDKSNKALSKPDDGDMTPASMEQENKAKMIX 296
OY      360 RPMAGDPCNGNLQANGAGSSSLGIDAMAGDAINMALGKGLAA 403
Db      297 SAVAGDPTGNTMLNLGAGGASLGIDAAVYGRKIANMSLGKLANA 340

RESULT 4
YA68_MYCTU STANDARD: PRT: 463 AA.
AC 053416;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PE-PGRS family protein Rv1068c.
GN Rv1068c OR MT1097 OR MY017.21C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishel W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (Apr-2001) to the EMBL/Genbank/DBD databases.
RN [1] SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
SUBFAMILY.
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DR EMBL: AL021897; CAI17184.1; -.
DR EMBL: AE006991; AAK45353.1; ALT_INIT.
DR TIGR: MT1097; -.
DR Tuberculist: Rv1068c; -.
DR InterPro: IPR000084; PE_region.
DR Pfam: PF00934; PE_1.
DR ProDom: PD001223; PE_region; 1.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 218 218 T -> S (IN REF. 2).
FT CONFLICT 235 235 G -> GGGAGTGGAGDGTGKSGAGAGAGAGAGTGHGCV
FT GGDGTGGTGGGCGGCGVGEPPDTRAGAGAG (IN REF.
SQ SEQUENCE 463 AA; 39305 MW; CF5696A7E9393952 CRC64;

Query Match 11.9%; Score 248; DB 1; Length 463;
Best local Similarity 31.8%; Pred. No. 3.7e-08;
Matches 93; Conservative 17; Mismatches 112; Indels 70; Gaps 13;

OY 8 LGASTMQISIGAGGNNGLGTSRONAGLGNSALGLGAGNONDTYVNLGLLTGMMMA 67
Db 203 IGAPVAGAGAGAGAGTAGLFG-----NGAGAGAGAGAGAGRGGD--GGSAGMLSGNGDA 256
OY 68 SMNGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLG 127
Db 257 GTGGGGGAGNAGNGGAGSAGMLSGNGGTGGC-----GTTAGA--GGGGNG--NS 301
OY 128 PLDQALGINSTGNDSTGTDSTSDSDPMQQLKMFSEIMQSLFGDQDGTGSS--- 184
Db 302 GIDPG---NGGGADPTGNNNGNGHGSA-----AKLFGDAGAGAGAGMST 344
OY 185 -----SGKOPTGEQNAKKGYVDALSGLMGNGLSQLL---GNGGLGCGGCG--G 229
Db 345 GTGGGGGGRGFGGCGGNGGNGHAGAGSGGTAGLILSGSGGTGGDGGNGGLGAGAGK 404
OY 230 NGGTGDSGLGKQNLGSPVYDQQLGNNVGTGIGKAGIOLALNDLGTNRHSRSPYNNK 278
Db 405 NGSNGGD---GKG-----GDAQLLNGGNGGNGGGLGMLGMLNGTG 445

RESULT 5
Y034_MYCTU STANDARD: PRT: 778 AA.
ID Y034_MYCTU
AC P11933;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PE-PGRS family protein Rv2634c.
GN Rv2634c OR MT2712 OR MYC1441.04C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CDC 1551 / Oshkosh;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

```

[illegible]

QY 255 QOLGNVGTG-----IGMKAGIOALNDIGTHRSSTFRSPVFKGDRAMAKEIGQFMDQY 308  
 Db 631 SLIGSGGTGNGNGNSIGV-AGIGGAGRG-----GDAGL-----664  
 QY 309 EVFKPKQYKQPGQEVKTDKSNAKALSKRPDDDKMTSPASMDQFNKAKMKIRPMAGDTGN 368  
 Db 665 -LFG-----AACTGG-----HQAAGVPAVGAGGAGCN 690  
 QY 369 GNLQARGAGSSIGIDAMAGDAINNMALGKIG 401  
 Db 691 GGLFANGAGAGAGGAFNA-AGGNGNGIGLFTGIG 722

RESULT 7  
 Y140 MYCTU STANDARD: PRT: 515 AA.  
 AC Q50594:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical PE-PGRS family protein RV1840C.  
 GN RV1840C OR MT1888 OR MTCY1A11.04 OR MTCY359.33.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteriales; Actinobacteria (class); Actinobacteridae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID-1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV:  
 RA MEDLINE-96295987; PubMed-9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ernolova M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 [1]  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Z83859; CAB06114.1; -  
 DR EMBL: AE007047; AAK46159.1; -  
 DR TIGR: MT1888; -  
 DR TubercuList: RV1840C; -  
 DR InterPro: IPR000084; PE\_region.  
 DR Pfam: PF00934; PE\_1.  
 KW Hypothetical protein, Transmembrane, Complete proteome.  
 FT TRANSMEM 1 21 POTENTIAL.

FT TRANSMEM 165 185 POTENTIAL.  
 FT TRANSMEM 199 219 POTENTIAL.  
 SQ SEQUENCE 515 AA; 43916 MW; 2EDC086C6D28B7F3 CRC64;  
 Query Match 11.5%; Score 238.5; DB 1; Length 515;  
 Best Local Similarity 27.3%; Pred. No. 1.5e-07;  
 Matches 109; Conservative 23; Mismatches 128; Indels 139; Gaps 15;  
 QY 18 GGAGNNGLTGRNRNAGIGNSALGIGGNGNDVNVNLAGLTTGMMAMMSMGGGG 77  
 Db 148 GGAGGDPAGLITGNG-GNGIGGPGATGAG-----AGGVGLITGDDGNGGAGG 197  
 QY 78 GGLGGGLGNGLGSGGLGEGLSNALNDMIGSLNTLGSKGNNTTSTNSPL--DQALGI 135  
 Db 198 TGPVGATG-GIGGPGGAAYGLFHHGAGAGAGGLGKAGAFGAGGAGTGGILYXGNGNG 256  
 QY 136 NSTSONDSTSGTSDTSDSDPMOOLLKMFSEIMOSLFEGDGTGSGSSGGKPTBEBQ 195  
 Db 257 NTPSGAADGAGGDA-----RLTNGCGDG-----GSVGAAPLTG--- 289  
 QY 196 NAYKKGYTDALSGINGNLSQLNGNGIGG-----GGGNNAGTGLDSSSLGKGLQNLSPV 252  
 Db 290 -----TNG-----GNGNGGLTYLGGSGSGLTGGPSDGTG----- 322  
 QY 253 DYQULGNNAVGTGIGMKAGIOALNDIGTHRSSTFRSPVFKGDRAMAKEIGQFMDQY 312  
 Db 323 -----GNMGPFDDGGGFSFPDNGGCGGTGTLTNGCGD----- 358  
 QY 313 KFOYKQPGQEVKTDKSNAKALSKRPDDDKMTSPASMDQFNKAKMKIRPMAGDTGN 368  
 Db 359 -----GGSNVOTD-----GFL-RHGSDGNNAVGL 382  
 QY 369 -GNLQARGAGSSIGIDAMAGDAINNMALGKIG 402  
 Db 383 IGMGAGGAGSAGTGFAPGGSGGNGGALLVNGGA 421

RESULT 8  
 Y208 MYCTU STANDARD: PRT: 1901 AA.  
 AC Q53553;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical PE-PGRS family protein RV3508 precursor.  
 GN RV3508 OR MTCV23.15.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteriales; Actinobacteria (class); Actinobacteridae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID-1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV:  
 RA MEDLINE-96295987; PubMed-9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 [1]  
 CC -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS  
 CC SUBFAMILY.  
 CC -----  
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**OY**    298 KEIGGFQMOYPEVFGKPOYOAGGGEVKTDKSMARALKSPDDGGATPASMEOFNNAKG     356  
      :|:::~::~||-|-----  
**Dd**    513 QDILSFNIEPTALTRPLIGN-----DSCTPGTGD-GGAGG     550





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DR EMBL; AL021958; CAA17514.1; -
DR EMBL; AE006968; AAK45011.1; -
DR TIGR; MT0772.5; -
DR Tuberculist; Rv0747; -
DR InterPro; IPR000084; PE_region
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RP SEQUENCE FROM N.A.  
RC STRAIN-H37R;  
RX MEDLINE-9825987; PubMed-9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Church C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tenaka F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,



FT CONFLICT 312 312 G -> GG (IN REF. 1)  
 SQ SEQUENCE 491 AA; 41979 MW; 12C8630C59CA0C13 CRC64;  
 Query Match 11.0%; Score 229; DB 1; Length 491;  
 Best Local Similarity 29.2%; Pred. No. 5.3e-07;  
 Matches 106; Conservative 22; Mismatches 149; Indels 86; Gaps 17;  
 QY 9 GASTM0ISIGAGGNNGLGTSRONAGLGSNLSALGCGNONTVNOAGL----- 60.  
 DB 145 GSTSPGVAGAGSAGLIG-----NGRGNGAPAGGAGN-----GGLGGLLNGGAGG 195  
 QY 61 -----TGMMMMMSHGGGGLMGCGLIG-----GLNGLGSGGGLG 95  
 DB 196 VGTGTNGYVDLGGAGGGGDDGLGAGLIGHGAGNGDGGHGGSGKAGSGSGGFG 255  
 QY 96 EGLSNALNDMLGSLTLTASRGKNNNTSTNSPLDQALGINSTS--ONDDSTSGT--DSTS 152  
 DB 256 Q--FGGAGGLYXNGAGS--GGNGDAGTGVSSDPAFLGSGGCGNDAGLIGVGCGG 312  
 QY 153 DSDP--MOOLKMESE-----IMSLFGDQDGTGSSSGSKOPTGEGONAYKKGVTA 205  
 DB 313 NGDDPILGRLFPVGRGDKGVGWLXGDKGGCGGNGG--LPFISTNA----- 362  
 QY 206 LSLGMLNGLS-OLLGNGLGGGCGGNAGTGLDSSSLGKGLNLGSPVDYQOLGNVCTG 264  
 DB 363 -----GNGSARLIGNAGAGSGSGAPGSVSGVGAGNPGSGNGGVMYNG--GAG 416  
 QY 265 IGMKAGIALNDI-----GTHRSSTRSFVNGDRAMAKEIGFMDQYEVFGKPYOK 318  
 DB 417 GAAGCGGPGMNTTSPGPGVGHGHTALIFDGAGAGAGAACG-----P---GTPDGA 468  
 QY 319 GPG 321  
 DB 469 GPG 471  
 RESULT 15  
 GRPL\_PETHY STANDARD; PRT; 384 AA.  
 AC P09789;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, last sequence update)  
 DT 01-AUG-1992 (Rel. 23, last annotation update)  
 DE Glycine-rich cell wall structural protein 1 precursor.  
 GN GRP-1.  
 OS Petunia hybrida (Petunia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.  
 OX NCBI\_TaxID=4102;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Condit C.M., Meagher R.B.;  
 RT \*A gene encoding a novel glycine-rich structural protein of petunia.\*;  
 RL Nature 323:178-181(1986).  
 CC -1- FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE CELL WALL (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Cell wall (potential).  
 CC -1- MISCELLANEOUS: THIS PROTEIN CONTAINS 67% GLYCINE RESIDUES.  
 CC -1- MISCELLANEOUS: 90% OF THE MATURE PROTEIN RESIDUES ARE CAPABLE OF  
 CC FORMING A BETA-PLEATED SHEET COMPOSED OF 8 ANTI-PARALLEL STRANDS.  
 CC -1- MISCELLANEOUS: THE GLYCINE-RICH REGION IS COMPRISED OF TWO RELATED  
 CC FAMILIES OF REPEATS, F1 AND F2, EACH REPEAT CONTAINING ABOUT 40  
 CC AA.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; X04335; CAA27866.1; -

DR PIR; A26099; A26099.  
 KW Cell wall; structural protein; Repeat; Signal.  
 FT SIGNAL 1 27  
 FT CHAIN 28 384 GLYCINE-RICH CELL WALL STRUCTURAL  
 FT DOMAIN 41 384 GLY-RICH.  
 SQ SEQUENCE 384 AA; 28777 MW; C8541C549417D18C CRC64;  
 Query Match 10.3%; Score 214.5; DB 1; Length 384;  
 Best Local Similarity 28.1%; Pred. No. 3e-06;  
 Matches 77; Conservative 17; Mismatches 111; Indels 69; Gaps 9;  
 QY 7 GLGASTM0ISIGAGGNNGLGTSRONAGLGSNLSALGCGNONTVNOAGLITGMM 66  
 DB 152 GFGAG-----GGVGGAGAGAGGVGGGGGGGGGGGGGGGGGGGGGGGGGGGG 201  
 QY 67 MSMMGGGLMGCGGLGGLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 126  
 DB 202 ---GAGGGLGGGVGG 243  
 QY 127 SPLDQALGINSTSONDDSTGTDSTSDSPMQLLKMFSEIMSLFGDGD-----GTQ 181  
 DB 244 -----GVGGGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 280  
 QY 182 GSSSGGKOPTGEBQMAKKVTDALSGLMNGLSOLLGNGLGGCGGAGNAGTGL--DGSS 239  
 DB 281 GGVGGGAAGGVGG 335  
 QY 240 LGKGLGLNLSGPDYQOLGNVCTGTMKRGIOA 273  
 DB 336 GGGGGIGGGHGG-----GFGVGVGIGIGVGVA 363

Search completed: June 12, 2003, 08:49:31  
 Job time : 14 secs



Db 110 -TTGAGS-----LGLDPTQTGDDSLSGAGQTSNMS-PMEQLMKIFADITQSLFGD-QDG 161  
 QY 180 TCGSSSGGKOPTGEGEONAYKGYTDALSGIMNGLSQLLNGGLGGGQGNAGTGLDSS 239  
 Db 162 ASGSGN-GKOPSGDEONAYKGYTDALTAEMGGGLSQVAGNSEGGLDGG-MGLG-GGNG 218  
 QY 240 LGGKGLONTSGPDYQOOLGNNAVGTGIGMKGIALNDIGHRSSSTRSPFNKGDRAK 299  
 Db 219 LGGKGLQDLSGPDYQOOLGNNAVGTGIGMKGIALNNIGHSSTRSPFNKEDRALARE 278  
 QY 300 ICGFMQYEFVEFGKPYOKPGQEVETDCKSNKALSKPDDGMPASMEQFNKAGMK 359  
 Db 279 VQGFMDQYEFTEKPYOKNADSAVYTDKSNKALSKPDDGMPASMEQFNKAGMK 338  
 QY 360 RPAAGDTGNGNLQARGAGSSSLGIDAMAGDAINNALGKIGAN 403  
 Db 339 SAMAGDNGNINLQARGAGSSMIGDITLGTDAINNALTRLSAA 382

## RESULT 2

ID 09KH45 PRELIMINARY; PRT; 365 AA.  
 AC 09KH45;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Harpin.  
 GN hrpN.  
 OS Pantoea agglomerans pv. gypsophillae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Pantoea.  
 OX NCBI\_TaxID=48984;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-21171042; PubMed-11277443;  
 RA Mor H., Manulis S., Zuck M., Nizan R., Coplin D.L., Barash I.;  
 RT Genetic organization of the hrp gene cluster and *desA*/*Br* operon in  
 RT *Erwinia herbicola* pv. *gypsophillae*.  
 RL Mol. Plant Microbe Interact. 14:431-436(2001).  
 DR EMBL; AF271716; AAF76342.1;  
 SQ SEQUENCE 365 AA; 36784 MW; 6F79BBDD95AC2A CRC64;

Query Match 48.2%; Score 1002.5; DB 2; Length 365;  
 Best Local Similarity 57.9%; Pred. No. 3.4e-50;

Matches 223; Conservative 40; Mismatches 83; Indels 39; Gaps 14;

QY 1 MSINTSGLGASTWQISIGGAGNNGILGTSRONAGLGSNSALGLGGGNONDYVNOIAGL 60  
 Db 1 MSINTPLGIPAMQISL---GDSNGILGPMLONAVNL-----SKGDSIDETINOLAGAL 52  
 QY 61 TGMAMMSMAGGGLMGGLGGGLGGLG--SGGLGEGISNALNDMGAGSLNT-LGSKG 117  
 Db 53 TAMMMAMMAGGSGL-GGGIGLTRA-GGELGQSGGALGGPLYGNGGQIGALGTSIGTG 110  
 QY 118 GNNITSTNSPLDQALGINSTSGNDSTSGTSTSS-----DPMQILLKMSSEIMOSL 172  
 Db 111 G-----ASSSLDKALDL-----DPTLDGGGLSSNGTGYGSPIDQILKMALEWQSM 157  
 QY 173 FEDGQDGTGSSGGRQPTGEGONAYKGYTDALSGIMNGLSQLLNGGLGGGQGNAG 232  
 Db 158 FG-GQGDITSGRGT-GNQPTPDQONATKGYTDALTAVMGGLSQMGGS-GTGGGANGSIG 214  
 QY 233 TGLDSSLGKGLQNTSGPDYQOOLGNNAVGTGIGMKGIALNDIGTHRSSSTRSPVNGK 292  
 Db 215 L---GNGLGKGLQELGNPADYEQLVGVTGVMAGIEALNNIGTESSTRTEFNKD 271  
 QY 293 DRMAKEIGOFMDQYEFVEFGKPYOKPGQEVETDCKSNKALSKPDDGMPASMEQFN 352  
 Db 272 DMSLAEGVQFMDQYEFTEKPYOKNADSAVYTDKSNKALSKPDDGMPASMEQFN 331  
 QY 353 KAKGMIKRPAGDTGNGNLQARGAG 377  
 Db 332 KAKGMIKSNMEGDT--GNLQATGEG 354

## RESULT 3

ID 093FY8 PRELIMINARY; PRT; 356 AA.  
 AC 093FY8;  
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DE hrpN.  
 GN hrpN.  
 OS Pectobacterium carotovorum subsp. carotovorum.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Pectobacterium.  
 OX NCBI\_TaxID=555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SCC1;  
 RA Rantakari A., Viitaharju O., Vaehaemiko S., Taira S., Palva T.E.,  
 RA Saarilahti H.T., Romanetschuk M.;  
 RT "Type III secretion contributes to the pathogenesis of soft-rotting  
 RT plant pathogen *Erwinia carotovora*: Partial characterization of the hrp  
 RT gene cluster."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF302656; AAK97283.1;  
 SQ SEQUENCE 356 AA; 35534 MW; 154C9D885810DCB8 CRC64;

Query Match 40.4%; Score 840.5; DB 2; Length 356;  
 Best Local Similarity 48.6%; Pred. No. 6.4e-41;

Matches 198; Conservative 36; Mismatches 114; Indels 59; Gaps 11;

QY 3 LNTSGLGASTWQISIGGAGNNGILGTSRONAGLGSNSALGLGGGNONDYVNOIAGL 61  
 Db 2 LNTSGGAS-LQITI-KAGNGGLTFPSSQNGSGSPQSAF---GGORSNIAEQLSDIT 56  
 QY 62 GMMAMMSMAGGGLMGGLG-----GGLGNGLGSGGLGEGISNALNDMGAGSLNTG 115  
 Db 57 TMFMGSMAGG--MSGGLGGLGSLGGLGGLG--GGLGGLGSSLSGSLGSLG--GG 111  
 QY 116 KGNNTSTNSPLDQALGINSTSGNDSTSGTSTSSDSDPMQILLKMSSEIMOSLFGD 175  
 Db 112 LGG-----ALGAGNANMNSAMGS-----LTFSLIEDLGG 143  
 QY 176 GQDGTGSSGGRQPTGEGONAYKGYTDALSGIMNGLSQLLNGGLGGGQGNAGTGL 235  
 Db 144 GMSQDQGGGLFNGNQPSSPELSATVGTGVNDLSAILNGLSQTRGQ-----T 189  
 QY 236 DGSGLGKGLQNTSGPDYQOOLGNNAVGTGIGMKGIALNDIGTHRSSSTRSPVNGRA 295  
 Db 190 SPLQGNNGIGLGSAGAFNQSLGSLMSYGRAGLQELNNISTHNDSPRYFYKEDRG 249  
 QY 296 MAKEIGOFMDQYEFVEFGKPYOKPGQEVETDCKSNKALSKPDDGMPASMEQFNKAK 355  
 Db 250 MAKEIGOFMDQYEFTEKPYOKNADSAVYTDKSNKALSKPDDGMPASMEQFNKAK 309  
 QY 356 GMIKRPAGDTGNGNLQARGAGSSSLGIDAMAGDAINNALGKIGAN 402  
 Db 310 GMITAVAGDTGNTLSARGNGASLIGIDAMIGDRVNMGLKISS 356

## RESULT 4

ID 09EXP0 PRELIMINARY; PRT; 344 AA.  
 AC 09EXP0;  
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)  
 DE Harpin protein.  
 GN hrpN.  
 OS *Erwinia chrysanthemi*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Pectobacterium.  
 OX NCBI\_TaxID=556;



OY 257 LGNAVGTGIGMKAGTGLDNDIGTHRSSTRSPVKNKDRAMAKETGPMQIPEVPEKPPOT 316  
 DB 1214 -GNA-----GIG-----GDGSGGNGCG-GDSGSGIGCGP 1243  
 OY 317 OKPGQEVETDCKSNKALSKPDDDMTPASMEQFKAKGIMKRPVAGPTGNGNLQARGA 376  
 DB 1244 AGPRG-----KGGAGNAGTGTGNGSGA 1267  
 OY 377 GGSGLIDAMMAGDAINNALKRLG 401  
 DB 1268 GGAGGCGAGAGAGISFSGNSNGGTG 1292

## RESULT 7

OY 007224 PRELIMINARY; PRT; 591 AA.  
 ID 007224  
 AC 007224;  
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE Hypothetical protein RV0297.  
 GN RV0297 OR MTCY63.02.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID-1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE-98295987; PubMed-9634230;  
 RA Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Cole S.T., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultston J.E., Taylor K., Whitehead S., Barrett B.G.,  
 RT "Deciphering the Biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 DR EMBL: Z96800; CAB09596.1;  
 DR Tuberculist: RV0297;  
 DR InterPro: IPR000084; PE\_region.  
 DR Pfam: PF00934; PE\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 591 AA; 49058 MW; 4E4675ED4297F5A CRC64;

Query Match 12.3%; Score 255; DB 16; Length 591;  
 Best Local Similarity 26.8%; Fred. No. 4e-07;

Matches 123; Conservative 24; Mismatches 168; Indels 144; Gaps 20;

OY 7 GLGASTMQISIGGAGNNGILGTSRONAGIGNSALGIGGNDVYNOLAGILTGMMMM 66  
 DB 141 GNGSGAPGQAGAGAGATGFFG-----NGNGGDCGAGANGC-----AGGTAGMFFG 187  
 OY 67 MSMAGGGGLMG-----GIGCGGIGLN-----GIGSGGIGLEISNALNDML----- 106  
 DB 188 FGNGGAGGIGVAGINGLGGAGGCGNAGFFGNGGNGGAGAGAVNANVNGLATPVT 247  
 OY 107 -----GSLNTLGSKG--GNNTTSTNSPLDQALGINSTQNDSTSG-----TDSSTDS 154  
 DB 248 PAANGNGNLVGPVPTAGGADGANGSALGQAGAGGCGDGNASTSGIGTIAOTGAGGA 307  
 OY 155 SDPMQOLLKMFSEIMSLFQDGODGTGSSSGGKOPTEBQNAKKGVTDALSGMNGNL 214  
 DB 308 G-----GAGDGAAPGNGNGGVSVEHT-----GATGS-SASGNGA 342  
 OY 215 SOLLNGGLG-----GGGNGACTGLDSSLGSKGLQNTSGPV 252  
 DB 343 TG--GNGGVGAPGAGGNGGNGHVSNGSVNTAGAGGKGGNGGTGAGGP--GGHGGSVLSGPV 399  
 OY 253 DYQOLGNAVGTGIGMKAGTGLDNDIGTHRSSTRS-----PVNKGDRAMAKETGPMQIPEV 308

DB 400 GDSGNGAGAGDG---GAGVSATDIAGTGRGNGNGHGLWIGNGCGAGAGV----- 449  
 OY 309 EFVFKPQYOKPGQEVETDCKSNKALSKPDDDMTPASMEQFKAKGIMKRPVAGPTGNGNLQARGA 376  
 DB 450 -----GVC-----GAGAGATGHHGGG-----GSVNTPIGSEAG 480  
 OY 365 DTGNGNLQARGAGSSSLGIDAMMAGDAINNALKRLGAA 403  
 DB 481 DGGKGGIGDGGGRGRTG--QPGAGAGAGAGVGGAGAGA 517

## RESULT 8

OY 08VKN3 PRELIMINARY; PRT; 622 AA.  
 ID 08VKN3  
 AC 08VKN3;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE PE\_PGRS family protein.  
 GN MT0311.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID-1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / OSHKOSH;  
 RA Rietschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Hatt D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uitterback T., Weidman J., Khoult H., Gill J., Mikula A.,  
 RA Bishop W.,  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE006938; AAK44534.1;  
 DR TIGR: MT0311;  
 DR InterPro: IPR00104; Antifreeze\_1.  
 DR InterPro: IPR000084; PE\_region.  
 DR Pfam: PF00934; PE\_1.  
 DR PRINTS: PRO0308; ANTIFREEZE1.  
 SQ SEQUENCE 622 AA; 52747 MW; B27AD977A4DE8D67 CRC64;

Query Match 12.2%; Score 254; DB 16; Length 622;  
 Best Local Similarity 27.5%; Fred. No. 4.8e-07;

Matches 125; Conservative 22; Mismatches 172; Indels 136; Gaps 20;

OY 7 GLGASTMQISIGGAGNNGILGTSRONAGIGNSALGIGGNDVYNOLAGILTGMMMM 66  
 DB 172 GNGSGAPGQAGAGAGATGFFG-----NGNGGDCGAGANGC-----AGGTAGMFFG 218  
 OY 67 MSMAGGGGLMG-----GIGCGGIGLN-----GIGSGGIGLEISNALNDML----- 106  
 DB 219 FGNGGAGGIGVAGINGLGGAGGCGNAGFFGNGGNGGAGAGAVNANVNGLATPVT 278  
 OY 107 -----GSLNTLGSKG--GNNTTSTNSPLDQALGINSTQNDSTSG-----TDSSTDS 154  
 DB 279 PAANGNGNLVGPVPTAGGADGANGSALGQAGAGGCGDGNASTSGIGTIAOTGAGGA 338  
 OY 155 SDPMQOLLKMFSEIMSLFQDGODGTGSSSGGKOPTEBQNAKKGVTDALSGMNGNL 214  
 DB 339 G-----GAGDGAAPGNGNGGVSVEHT-----GATGS-SASGNGA 373  
 OY 215 SOLLNGGLG-----GGGNGACTGLDSSLGSKGLQNTSGPV 252  
 DB 374 TG--GNGGVGAPGAGGNGGNGHVSNGSVNTAGAGGKGGNGGTGAGGP--GGHGGSVLSGPV 430  
 OY 253 DYQOLGNAVGTGIGMKAGTGLDNDIGTHRSSTRS-----PVNKGDRAMAKETGPMQIPEV 312  
 DB 431 GDSGNGAGAGDG---GAGVSATDIAGTGRGNGNGHGLWIGNGCGAGAGV----- 473  
 OY 313 KPQYOKPGQEVETDCKSNKALSKPDDDMTPASMEQFKAKGIMKRPVAGPTGNGNLQARGA 376

Db 474 -----GGVGGVGGVGGAGAGAGAGGCGD-----GSVMTPIGSGEAGDGK 515  
QY 369 GNLQAGAGSSSLGIDAMAGDALNNMAGKLGAA 403  
Db 516 GGLGGGGGGGRTG--QFGAGAGAGAGVGGAGCA 548

## RESULT 9

Q8VJ19 PRELIMINARY; PRT; 628 AA.  
ID 08VJ19  
AC 08VJ19  
DT 01-MAR-2002 (TREMblrel. 20, Created)  
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE PE\_PGRS family protein.  
GN MT3476.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN= CDC 1551 / OSHROSH;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwin M.L., Halt D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT \*Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A8007154; AAK47814.1;  
DR TIGR: MT3476;  
DR InterPro: IPR000104; Antifreeze\_1.  
DR InterPro: IPR001343; Hemlysn\_Ca\_bind.  
DR InterPro: IPR000084; PE\_region.  
DR InterPro: IPR002173; PfkB.  
DR Pfam: PF00934; PE; 1.  
DR PRINTS: PRO0308; ANTIFREEZE1.  
DR PRINTS: PRO0313; CABINDGRPT.  
DR ProDom: PD001223; PE\_region; 1.  
DR PROSITE: PS00583; PFKB\_KINASES\_1; UNKNOWN\_1.  
SQ SEQUENCE 628 AA; 53828 MW; 9F62B1E7CC2C567E CRC64;

Query Match 12.1%; Score 251.5; DB 16; Length 628;  
Best Local Similarity 30.6%; Pred. No. 6.8e-07;  
Matches 118; Conservative 16; Mismatches 155; Indels 97; Gaps 21;

QY 18 GGAGG--NNGLLGTSRQNALGAGNSALGAGGNDVTYNOLAGLLTGMNMMNMGGGL 75  
Db 320 GGAGGANGNRPAMTSTIANAGAGNGAAG--GDGANGAGAGAGGAAAGSSVGDDGNGG 378  
QY 76 MCG-----GLGGGAGNGAGSGGGLGEG--SNALNDMLGSLNTLASKGGNNTTSTTNSPLD 130  
Db 379 AGGTGTNGHAGGAG--GAGGAGGGRGMLVNGNGNGNGNG--GAAGNGAIGCTGC-- 430  
QY 131 QALGINSTGNDSTSGTSDTSSDPMQLKMFSLMSTLFDGDDGTGTGSSSGKRP 190  
Db 431 -AGGV--PANGGNSALGT-----QPVGGDGGGGNGGTG-- 463  
QY 191 TGEQONAYKKGVTDALSG--LMGNCISQLLNGGGLG--GGGAGNGTGLDSSSLGKGLQN 247  
Db 464 TGRGGRGGGSGGAGAGSAGMLMGNGNG--GNGGTGSGGAGGNGGIGDDAG--GGNATST 520  
QY 248 LSGPVDTQQLGNAVGTGIGKAGTIALNDIGTHRHSTSTFVNGDRAMAKETGOFMDQY 307  
Db 521 SSTPFDVHG--GNG--GAGGDAG-----HGTTGDKGDDGAGTGGRGGL-- 562  
QY 308 PEYFGKPYQKGGQEVKTDDKSWAKALSKRPDDGKMTPASMEQNKAKGATKRMAGDTG 367  
Db 563 -----AGQHRANSNGGGGGGTGAGAGTGG--TPGSGN-----AGTGTG 596

QY 368 NGLQAGAGSSSLGIDAMAGDALN 393  
Db 597 TGNADSTNGGPGSDG-----LGDAFN 618

## RESULT 10

Q8VX71 PRELIMINARY; PRT; 635 AA.  
ID 08VX71  
AC 08VX71  
DT 01-MAR-2002 (TREMblrel. 20, Created)  
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE PE\_PGRS family protein.  
GN MT1123.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN= CDC 1551 / OSHROSH;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwin M.L., Halt D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT \*Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains";  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: A8006992; AAK45381.1;  
DR TIGR: MT1123;  
DR InterPro: IPR000084; PE\_region.  
DR Pfam: PF00934; PE; 1.  
DR ProDom: PD001223; PE\_region; 1.  
SQ SEQUENCE 635 AA; 51726 MW; A461A61100C7C5D4 CRC64;

Query Match 12.0%; Score 250; DB 16; Length 635;  
Best Local Similarity 27.2%; Pred. No. 8.3e-07;  
Matches 120; Conservative 23; Mismatches 152; Indels 146; Gaps 20;

QY 7 GLGASTMQISTGGAGGNGLLGT---SRQNALGAGNSALGAGGNDVTYNOLAGLLTGM 63  
Db 293 GSGGHALLMGAGGAGGNGSGGTGAGAGNGAGGCGGT-----GGLIFG- 343  
QY 64 MAMMSMGGGGLMG-----GGLG--NGLGSGGGLGEGLSNALNDMLG 107  
Db 344 -----NGAGGCGATAGAGAGANGVSTYNGGTGNGGIGGTGSGAGAGN--GILG 395  
QY 108 -----GSLNTLASKGGNNTTSTTNSPLDQALGINSTQNDDSTSGTSDSSDPMQ 160  
Db 396 VGAGAGGASGAGDADRAGAGTGTSS--DGGAGGDDGGDNGAGAGTGG-- 444  
QY 161 LKMFSEIMOSLFDGDDGTGTGSSSGGKOPTGSDNAYKKGVTDALSGLMGNG----- 213  
Db 445 -----LFGAGNGNGGPG--GSGGAADIGGNGAGNGGCTDNGNGSGSGGAGSGG 492  
QY 214 -----LSQLLNGGL--GGGAGGN--AGTGLDSSSLGAGLONTLSGPVDYQQLGNAV 262  
Db 493 DGGAGGNGAALFNGAGGAGGGRGKNGAGAGGLGGGFFGLPGL--NGSG-----GPGC 544  
QY 263 TGIGMKAGTQALNDIGTHRHSTSTFVNGKGRBAKKEIGQPMQYPEYFGKPYQKPGQ 322  
Db 545 GGNKAPGCVLYLNGN-----GAGGQSSGGTIG-----GPG- 573  
QY 323 EVKTDKSWAKALSKRPDDGKMTPASMQFNKAKMKRPMAGDTGNGNTQARGAGSSSLG 382  
Db 574 -----ATGAGAGKGGG-------DAQLLGDGNGNGAGAGTGTGTPG 610  
QY 383 IDAMAGDALNNMAGKLGAA 403  
Db 611 PGPGGSGGGLGLLFGQTGTA 631



RESULT 11  
 ID 08VJ15 PRELIMINARY; PRT; 775 AA.  
 AC 08VJ15;  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE PE\_PCRS family protein.  
 GN MT3495.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC\_1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE007155; AAK47832.1; -  
 DR TIGR; MT3495; -  
 DR InterPro; IPR000084; PE\_region.  
 DR InterPro; IPR002173; PfKB.  
 DR Pfam; PF00934; PE; 1.  
 DR ProDom; PD001223; PE\_region; 1.  
 DR PROSITE; PS00583; PFKB\_KINASES\_1; UNKNOWN\_2.  
 SQ SEQUENCE 775 AA; 65448 MW; 5256A18546EDD53 CRC64;  
 Query Match 12.0%; Score 250; DB 16; Length 775;  
 Best Local Similarity 28.7%; Pred. No. 1e-06;  
 Matches 96; Conservative 23; Mismatches 101; Indels 114; Gaps 15;  
 QY 2 SLMTSGASTWQISIGAGGNNGLTGRQ-----NAGLGGN-SALGIG 45  
 DB 446 SAGTGGVAGS-----GGTGGNAGLIGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAG 499  
 QY 46 G---GNQNDTVNQLAGLITGMAMMSMMGGGGLMGGLG-GGLG-----NGLGSGG 93  
 DB 500 GGLYGGGAGGAGGAGG-----GANIAGNGSDGAAHGAGGAGGAGGAGGAGGAGGAGGAG 552  
 QY 94 LEBGLSNALNDMLGSLNLTGSKGN-----NTSTNSPLD 130  
 DB 553 AGGNTAGRRADAIACT---GGDGGNGGNGGILLGNAGAGGAGGAGGAGGAGGAGGAGGAGG 608  
 QY 131 QALGINTSONDSTSGTSTSDSSPMQQLKMFETIMQSLFGDQDDTQSSSGGKOP 190  
 DB 609 GATGGGNGGAGAGGTGFTGSG-----GIGGNGAGGTGGNAG----- 646  
 QY 191 TEGEDNAVKKGYTDAL-----SGIMNGLSQLLNGGLG-GGQGNAGTGLDSSLAGK 243  
 DB 647 -----VALSVGSTGIGLGGNGSGGLGCGGSGSLFNGNGAGGAGVATGNGSGSGIGPASYG 701  
 QY 244 G-----LQNLGSPVDYQQLGNANVTGIGMKAG 270  
 DB 702 GGGGGAAGLAG-----QIGNGSGSGSGGAGG 730  
 RESULT 12  
 ID 08VJ15 PRELIMINARY; PRT; 1217 AA.  
 AC 08VJ15;  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE PE\_PCRS family protein.  
 GN MT3615.3.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]

OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC\_1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE007164; AAK47974.1; -  
 DR TIGR; MT3615; -  
 DR InterPro; IPR000084; PE\_region.  
 DR InterPro; IPR002173; PfKB.  
 DR Pfam; PF00934; PE; 1.  
 DR ProDom; PD001223; PE\_region; 1.  
 DR PROSITE; PS00583; PFKB\_KINASES\_1; UNKNOWN\_3.  
 SQ SEQUENCE 1217 AA; 94463 MW; 2F5BDC5A30A056E CRC64;  
 Query Match 12.0%; Score 249.5; DB 16; Length 1217;  
 Best Local Similarity 25.5%; Pred. No. 1.8e-06;  
 Matches 112; Conservative 27; Mismatches 148; Indels 153; Gaps 17;  
 QY 4 NTSGLGASTWQISIGAG-----CGNNGILGTSRONAGLGSNALSIG-----LGG 46  
 DB 731 NPTGIGTGIDGTGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 789  
 QY 47 GNQNDTVNQLAGLITGMAMMSMMGGGGLMGGLG-----GGLG--NGLGSGGIGLEG 97  
 DB 790 GADADPGATG--TGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 847  
 QY 98 LSNALNDMLGGS--LMTLTSKNGNNTSTNSPLDQALGINSQNDSTSGTSTSDSS 155  
 DB 848 FSRGSGGTGGTGGVGTGGTGGN-----AGGACDPKRGKGTGTGTGGSG 894  
 QY 156 DPMQQLKMFETIMQSLFGDQDDTQSS-----SGGKRPTEGONAKKRYTDALSG 208  
 DB 895 -----GAGSGGAGNNGT 934  
 QY 209 LKNGLSQLLNGGLG-----GQGNAGTGLDSSSLGKGLQNLGSPVDYQQLGNAY 261  
 DB 935 TGGTG-----GTGCKGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 983  
 QY 262 GTGIGKAGIQLANDIGTHHSSTRFVFKGDAAMKEIGQFPDQIPEYFGKFOYOKRG 321  
 DB 984 ---GIG-----GDSGGGNGGQ--GDSGSGLGQDGFAGGPG 1015  
 QY 322 QEVKTDKSWAKALSRPDDGKTPASWQFNNKAKIKRPMAGDTGNGNLQARGAGSSSL 381  
 DB 1016 G-----KGGAGGNAGT 1039  
 QY 382 GIDAMAGALNNMALGKIG 401  
 DB 1040 QGAGAGAGISFNSNGSGTG 1059  
 RESULT 13  
 ID 050415 PRELIMINARY; PRT; 731 AA.  
 AC 050415;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE PCRS-family protein.  
 GN RV3388 OR MTV004.46.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]



